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DEC 26 2001

TECH CENTER 1600,2900

SEQUENCE LISTING

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PETROUNIA, Ionna P.
SUN, Lianhong

<120> DIRECTED EVOLUTION OF OXIDASE ENZYMES

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<140> 09/722,602

<141> 2000-11-27

<150> US 09/571,553

<151> 2000-05-16

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35 40 45
Pro Lys Pro Pro His Thr Tyr Thr Ile Asp Met Lys Thr Thr Gln Asn
50 55 60
Val Asn Gly Leu Ser Met Leu Pro Arg Gln Asp Gly Asn Gln Asn Gly
65 70 75 80
Trp Ile Gly Arg His Glu Val Tyr Leu Ser Ser Asp Gly Thr Asn Trp
85 90 95
Gly Ser Pro Val Ala Ser Gly Ser Trp Phe Ala Asp Ser Thr Thr Lys
100 105 110
Tyr Ser Asn Phe Glu Thr Arg Pro Ala Arg Tyr Val Arg Leu Val Ala
115 120 125
Ile Thr Glu Ala Asn Gly Gln Pro Trp Thr Ser Ile Ala Glu Ile Asn
130 135 140
Val Phe Gln Ala Ser Ser Tyr Thr Ala Pro Gln Pro Gly Leu Gly Arg
145 150 155 160
Trp Gly Pro Thr Ile Asp Leu Pro Ile Val Pro Ala Ala Ala Ala Ile
165 170 175
Glu Pro Thr Ser Gly Arg Val Leu Met Trp Ser Ser Tyr Arg Asn Asp
180 185 190
Ala Phe Gly Gly Ser Pro Gly Gly Ile Thr Leu Thr Ser Ser Trp Asp
195 200 205
Pro Ser Thr Gly Ile Val Ser Asp Arg Thr Val Thr Val Thr Lys His
210 215 220
Asp Met Phe Cys Pro Gly Ile Ser Met Asp Gly Asn Gly Gln Ile Val

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<223> Mutant 9.16.6C11 (V494A, C515S) of D. dendroides
 GaO

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Pro	Lys	Pro	Pro	His	Thr	Tyr	Thr	Ile	Asp	Met	Lys	Thr	Thr	Gln	Asn	50	55	60	
Val	Asn	Gly	Leu	Ser	Met	Leu	Pro	Arg	Gln	Asp	Gly	Asn	Gln	Asn	Gly	65	70	75	80
Trp	Ile	Gly	Arg	His	Glu	Val	Tyr	Leu	Ser	Ser	Asp	Gly	Thr	Asn	Trp	85	90	95	
Gly	Ser	Pro	Val	Ala	Ser	Gly	Ser	Trp	Phe	Ala	Asp	Ser	Thr	Thr	Lys	100	105	110	
Tyr	Ser	Asn	Phe	Glu	Thr	Arg	Pro	Ala	Arg	Tyr	Val	Arg	Leu	Val	Ala	115	120	125	
Ile	Thr	Glu	Ala	Asn	Gly	Gln	Pro	Trp	Thr	Ser	Ile	Ala	Glu	Ile	Asn	130	135	140	
Val	Phe	Gln	Ala	Ser	Ser	Tyr	Thr	Ala	Pro	Gln	Pro	Gly	Leu	Gly	Arg	145	150	155	160
Trp	Gly	Pro	Thr	Ile	Asp	Leu	Pro	Ile	Val	Pro	Ala	Ala	Ala	Ala	Ile	165	170	175	
Glu	Pro	Thr	Ser	Gly	Arg	Val	Leu	Met	Trp	Ser	Ser	Tyr	Arg	Asn	Asp	180	185	190	
Ala	Phe	Gly	Gly	Ser	Pro	Gly	Gly	Ile	Thr	Leu	Thr	Ser	Ser	Trp	Asp	195	200	205	
Pro	Ser	Thr	Gly	Ile	Val	Ser	Asp	Arg	Thr	Val	Thr	Val	Thr	Lys	His	210	215	220	
Asp	Met	Phe	Cys	Pro	Gly	Ile	Ser	Met	Asp	Gly	Asn	Gly	Gln	Ile	Val	225	230	235	240
Val	Thr	Gly	Gly	Asn	Asp	Ala	Lys	Lys	Thr	Ser	Leu	Tyr	Asp	Ser	Ser	245	250	255	
Ser	Asp	Ser	Trp	Ile	Pro	Gly	Pro	Asp	Met	Gln	Val	Ala	Arg	Gly	Tyr	260	265	270	
Gln	Ser	Ser	Ala	Thr	Met	Ser	Asp	Gly	Arg	Val	Phe	Thr	Ile	Gly	Gly	275	280	285	
Ser	Trp	Ser	Gly	Gly	Val	Phe	Glu	Lys	Asn	Gly	Glu	Val	Tyr	Ser	Pro	290	295	300	
Ser	Ser	Lys	Thr	Trp	Thr	Ser	Leu	Pro	Asn	Ala	Lys	Val	Asn	Pro	Met	305	310	315	320
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Asp	Thr	Phe	Tyr	Lys	Gln	Asn	Pro	Asn	Ser	Ile	Val	Arg	Ala	Tyr	His
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Ser	Ile	Ser	Leu	Leu	Leu	Pro	Asp	Gly	Arg	Val	Phe	Asn	Gly	Gly	Gly
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Thr	Pro	Asn	Tyr	Leu	Tyr	Asn	Ser	Asn	Gly	Asn	Leu	Ala	Thr	Arg	Pro
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Thr	Ile	Ser	Thr	Asp	Ser	Ser	Ile	Ser	Lys	Ala	Ser	Leu	Ile	Arg	Tyr
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 GaO

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Gly	Asn	Lys	Asp	Thr	Phe	Trp	His	Thr	Phe	Tyr	Gly	Ala	Asn	Gly	Asp
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Pro	Lys	Pro	Pro	His	Thr	Tyr	Thr	Ile	Asp	Met	Lys	Thr	Thr	Gln	Asn
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Glu	Pro	Thr	Ser	Gly	Arg	Val	Leu	Met	Trp	Ser	Ser	Tyr	Arg	Asn	Asp
			180					185					190		
Ala	Phe	Gly	Gly	Ser	Pro	Gly	Gly	Ile	Thr	Leu	Thr	Ser	Ser	Trp	Asp
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				245					250					255	
Ser	Asp	Ser	Trp	Ile	Pro	Gly	Pro	Asp	Met	Gln	Val	Ala	Arg	Gly	Tyr
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Ser	Trp	Ser	Gly	Gly	Val	Phe	Glu	Lys	Asn	Gly	Glu	Val	Tyr	Ser	Pro
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Ser	Ser	Lys	Thr	Trp	Thr	Ser	Leu	Pro	Asn	Ala	Lys	Val	Asn	Pro	Met
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Leu	Thr	Ala	Asp	Lys	Gln	Gly	Leu	Tyr	Arg	Ser	Asp	Asn	His	Ala	Trp
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Leu	Phe	Gly	Trp	Lys	Lys	Gly	Ser	Val	Phe	Gln	Ala	Gly	Pro	Ser	Thr
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Ala	Met	Asn	Trp	Tyr	Tyr	Thr	Ser	Gly	Ser	Gly	Asp	Val	Lys	Ser	Ala
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Glu	Asp	Ser	Thr	Pro	Val	Phe	Thr	Pro	Glu	Ile	Tyr	Val	Pro	Glu	Gln

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Asp	Thr	Phe	Tyr	Lys	Gln	Asn	Pro	Asn	Ser	Ile	Val	Arg	Ala	Tyr	His
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Gly	Leu	Cys	Gly	Asp	Cys	Thr	Thr	Asn	His	Phe	Asp	Ala	Gln	Ile	Phe
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Thr	Pro	Asn	Tyr	Leu	Tyr	Asn	Ser	Asn	Gly	Asn	Leu	Ala	Thr	Arg	Pro
	530					535					540				
Lys	Ile	Thr	Arg	Thr	Ser	Thr	Gln	Ser	Val	Lys	Val	Gly	Gly	Arg	Ile
545					550					555					560
Thr	Ile	Ser	Thr	Asp	Ser	Ser	Ile	Ser	Lys	Ala	Ser	Leu	Ile	Arg	Tyr
				565				570						575	
Gly	Thr	Ala	Thr	His	Thr	Val	Asn	Thr	Asp	Gln	Arg	Arg	Ile	Pro	Leu
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Thr	Leu	Thr	Asn	Asn	Gly	Gly	Asn	Ser	Tyr	Ser	Phe	Gln	Val	Pro	Ser
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 dendroides GaO

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			20					25					30		
Gly	Asn	Lys	Asp	Thr	Phe	Trp	His	Thr	Phe	Tyr	Gly	Ala	Asn	Gly	Asp
		35					40					45			
Pro	Lys	Pro	Pro	His	Thr	Tyr	Thr	Ile	Asp	Met	Lys	Thr	Thr	Gln	Asn
	50					55					60				
Val	Asn	Gly	Leu	Ser	Met	Leu	Pro	Arg	Gln	Asp	Gly	Asn	Gln	Asn	Gly
65					70					75				80	
Trp	Ile	Gly	Arg	His	Glu	Val	Tyr	Leu	Ser	Ser	Asp	Gly	Thr	Asn	Trp
				85					90					95	
Gly	Ser	Pro	Val	Ala	Ser	Gly	Ser	Trp	Phe	Ala	Asp	Ser	Thr	Thr	Lys
			100					105					110		
Tyr	Ser	Asn	Phe	Glu	Thr	Arg	Pro	Ala	Arg	Tyr	Val	Arg	Leu	Val	Ala
		115					120					125			
Ile	Thr	Glu	Ala	Asn	Gly	Gln	Pro	Trp	Thr	Ser	Ile	Ala	Glu	Ile	Asn
	130					135					140				
Val	Phe	Gln	Ala	Ser	Ser	Tyr	Thr	Ala	Pro	Gln	Pro	Gly	Leu	Gly	Arg
145					150					155					160
Trp	Gly	Pro	Thr	Ile	Asp	Leu	Pro	Ile	Val	Pro	Ala	Ala	Ala	Ala	Ile

				165				170					175			
Glu	Pro	Thr	Ser	Gly	Arg	Val	Leu	Met	Trp	Ser	Ser	Tyr	Arg	Asn	Asp	
			180					185					190			
Ala	Phe	Gly	Gly	Ser	Pro	Gly	Gly	Ile	Thr	Leu	Thr	Ser	Ser	Trp	Asp	
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Pro	Ser	Thr	Gly	Ile	Val	Ser	Asp	Arg	Thr	Val	Thr	Val	Thr	Lys	His	
	210					215					220					
Asp	Met	Phe	Cys	Pro	Gly	Ile	Ser	Met	Asp	Gly	Asn	Gly	Gln	Ile	Val	
225					230					235					240	
Val	Thr	Gly	Gly	Asn	Asp	Ala	Lys	Lys	Thr	Ser	Leu	Tyr	Asp	Ser	Ser	
				245					250					255		
Ser	Asp	Ser	Trp	Ile	Pro	Gly	Pro	Asp	Met	Gln	Val	Ala	Arg	Gly	Tyr	
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Gln	Ser	Ser	Ala	Thr	Met	Ser	Asp	Gly	Arg	Val	Phe	Thr	Ile	Gly	Gly	
		275					280					285				
Ser	Trp	Ser	Gly	Gly	Val	Phe	Glu	Lys	Asn	Gly	Glu	Val	Tyr	Ser	Pro	
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Ser	Ser	Lys	Thr	Trp	Thr	Ser	Leu	Pro	Asn	Ala	Lys	Val	Asn	Pro	Met	
305					310					315					320	
Leu	Thr	Ala	Asp	Lys	Gln	Gly	Leu	Tyr	Arg	Ser	Asp	Asn	His	Ala	Trp	
				325					330					335		
Leu	Phe	Gly	Trp	Lys	Lys	Gly	Ser	Val	Phe	Gln	Ala	Gly	Pro	Ser	Thr	
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Ala	Met	Asn	Trp	Tyr	Tyr	Thr	Ser	Gly	Ser	Gly	Asp	Val	Lys	Ser	Ala	
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Gly	Lys	Arg	Gln	Ser	Asn	Arg	Gly	Val	Ala	Pro	Asp	Ala	Met	Cys	Gly	
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Asn	Ala	Val	Met	Tyr	Asp	Ala	Val	Lys	Gly	Lys	Ile	Leu	Thr	Phe	Gly	
385					390					395					400	
Gly	Ser	Pro	Asp	Tyr	Gln	Asp	Ser	Asp	Ala	Thr	Thr	Asn	Ala	His	Ile	
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Ile	Thr	Leu	Gly	Glu	Pro	Gly	Thr	Ser	Pro	Asn	Thr	Val	Phe	Ala	Ser	
			420				425						430			
Asn	Gly	Leu	Tyr	Phe	Ala	Arg	Thr	Phe	His	Thr	Ser	Val	Val	Leu	Pro	
	435						440					445				
Asp	Gly	Ser	Thr	Phe	Ile	Thr	Gly	Gly	Gln	Arg	Arg	Gly	Ile	Pro	Phe	
	450				455					460						
Glu	Asp	Ser	Thr	Pro	Val	Phe	Thr	Pro	Glu	Ile	Tyr	Val	Pro	Glu	Gln	
465					470					475					480	
Asp	Thr	Phe	Tyr	Lys	Gln	Asn	Pro	Asn	Ser	Ile	Val	Arg	Ala	Tyr	His	
				485				490						495		
Ser	Ile	Ser	Leu	Leu	Leu	Pro	Asp	Gly	Arg	Val	Phe	Asn	Gly	Gly	Gly	
			500					505					510			
Gly	Leu	Cys	Gly	Asp	Cys	Thr	Thr	Asn	His	Phe	Asp	Ala	Gln	Ile	Phe	
		515					520					525				
Thr	Pro	Asn	Tyr	Leu	Tyr	Asn	Ser	Asn	Gly	Asn	Leu	Ala	Thr	Arg	Pro	
	530					535						540				
Lys	Ile	Thr	Arg	Thr	Ser	Thr	Gln	Ser	Val	Lys	Val	Gly	Gly	Arg	Ile	
545					550					555					560	
Thr	Ile	Ser	Thr	Asp	Ser	Ser	Ile	Ser	Lys	Ala	Ser	Leu	Ile	Arg	Tyr	
				565				570						575		
Gly	Thr	Ala	Thr	His	Thr	Val	Asn	Thr	Asp	Gln	Arg	Arg	Ile	Pro	Leu	
			580					585					590			

Thr	Leu	Thr	Asn	Asn	Gly	Gly	Asn	Ser	Tyr	Ser	Phe	Gln	Val	Pro	Ser
		595					600					605			
Asp	Ser	Gly	Val	Ala	Leu	Pro	Gly	Tyr	Trp	Met	Leu	Phe	Val	Met	Asn
	610					615					620				
Ser	Ala	Gly	Val	Pro	Ser	Val	Ala	Ser	Thr	Ile	Arg	Val	Thr	Gln	
625					630					635					

<210> 14
 <211> 639
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Mutant 11.03.10C3 (A3, P136, G195E, V494A) of D.
 dendroides GaO

<400> 14

Ala	Ser	Ala	Pro	Ile	Gly	Ser	Ala	Ile	Ser	Arg	Asn	Asn	Trp	Ala	Val
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Thr	Cys	Asp	Ser	Ala	Gln	Ser	Gly	Asn	Glu	Cys	Asn	Lys	Ala	Ile	Asp
			20					25					30		
Gly	Asn	Lys	Asp	Thr	Phe	Trp	His	Thr	Phe	Tyr	Gly	Ala	Asn	Gly	Asp
		35					40					45			
Pro	Lys	Pro	Pro	His	Thr	Tyr	Thr	Ile	Asp	Met	Lys	Thr	Thr	Gln	Asn
	50					55					60				
Val	Asn	Gly	Leu	Ser	Met	Leu	Pro	Arg	Gln	Asp	Gly	Asn	Gln	Asn	Gly
65					70					75					80
Trp	Ile	Gly	Arg	His	Glu	Val	Tyr	Leu	Ser	Asp	Gly	Thr	Asn	Trp	
				85					90				95		
Gly	Ser	Pro	Val	Ala	Ser	Gly	Ser	Trp	Phe	Ala	Asp	Ser	Thr	Thr	Lys
			100					105					110		
Tyr	Ser	Asn	Phe	Glu	Thr	Arg	Pro	Ala	Arg	Tyr	Val	Arg	Leu	Val	Ala
		115					120					125			
Ile	Thr	Glu	Ala	Asn	Gly	Gln	Pro	Trp	Thr	Ser	Ile	Ala	Glu	Ile	Asn
	130					135					140				
Val	Phe	Gln	Ala	Ser	Ser	Tyr	Thr	Ala	Pro	Gln	Pro	Gly	Leu	Gly	Arg
145					150					155					160
Trp	Gly	Pro	Thr	Ile	Asp	Leu	Pro	Ile	Val	Pro	Ala	Ala	Ala	Ala	Ile
				165					170					175	
Glu	Pro	Thr	Ser	Gly	Arg	Val	Leu	Met	Trp	Ser	Ser	Tyr	Arg	Asn	Asp
			180					185					190		
Ala	Phe	Glu	Gly	Ser	Pro	Gly	Gly	Ile	Thr	Leu	Thr	Ser	Ser	Trp	Asp
		195					200					205			
Pro	Ser	Thr	Gly	Ile	Val	Ser	Asp	Arg	Thr	Val	Thr	Val	Thr	Lys	His
	210					215						220			
Asp	Met	Phe	Cys	Pro	Gly	Ile	Ser	Met	Asp	Gly	Asn	Gly	Gln	Ile	Val
225					230					235					240
Val	Thr	Gly	Gly	Asn	Asp	Ala	Lys	Lys	Thr	Ser	Leu	Tyr	Asp	Ser	Ser
				245					250					255	
Ser	Asp	Ser	Trp	Ile	Pro	Gly	Pro	Asp	Met	Gln	Val	Ala	Arg	Gly	Tyr
			260					265					270		
Gln	Ser	Ser	Ala	Thr	Met	Ser	Asp	Gly	Arg	Val	Phe	Thr	Ile	Gly	Gly
		275					280						285		

Ser	Trp	Ser	Gly	Gly	Val	Phe	Glu	Lys	Asn	Gly	Glu	Val	Tyr	Ser	Pro
290						295					300				
Ser	Ser	Lys	Thr	Trp	Thr	Ser	Leu	Pro	Asn	Ala	Lys	Val	Asn	Pro	Met
305					310					315					320
Leu	Thr	Ala	Asp	Lys	Gln	Gly	Leu	Tyr	Arg	Ser	Asp	Asn	His	Ala	Trp
				325					330					335	
Leu	Phe	Gly	Trp	Lys	Lys	Gly	Ser	Val	Phe	Gln	Ala	Gly	Pro	Ser	Thr
			340					345					350		
Ala	Met	Asn	Trp	Tyr	Tyr	Thr	Ser	Gly	Ser	Gly	Asp	Val	Lys	Ser	Ala
		355					360					365			
Gly	Lys	Arg	Gln	Ser	Asn	Arg	Gly	Val	Ala	Pro	Asp	Ala	Met	Cys	Gly
	370					375					380				
Asn	Ala	Val	Met	Tyr	Asp	Ala	Val	Lys	Gly	Lys	Ile	Leu	Thr	Phe	Gly
385					390					395					400
Gly	Ser	Pro	Asp	Tyr	Gln	Asp	Ser	Asp	Ala	Thr	Thr	Asn	Ala	His	Ile
				405					410					415	
Ile	Thr	Leu	Gly	Glu	Pro	Gly	Thr	Ser	Pro	Asn	Thr	Val	Phe	Ala	Ser
			420					425					430		
Asn	Gly	Leu	Tyr	Phe	Ala	Arg	Thr	Phe	His	Thr	Ser	Val	Val	Leu	Pro
		435					440					445			
Asp	Gly	Ser	Thr	Phe	Ile	Thr	Gly	Gly	Gln	Arg	Arg	Gly	Ile	Pro	Phe
	450					455				460					
Glu	Asp	Ser	Thr	Pro	Val	Phe	Thr	Pro	Glu	Ile	Tyr	Val	Pro	Glu	Gln
465					470					475					480
Asp	Thr	Phe	Tyr	Lys	Gln	Asn	Pro	Asn	Ser	Ile	Val	Arg	Ala	Tyr	His
				485					490					495	
Ser	Ile	Ser	Leu	Leu	Leu	Pro	Asp	Gly	Arg	Val	Phe	Asn	Gly	Gly	Gly
			500					505					510		
Gly	Leu	Cys	Gly	Asp	Cys	Thr	Thr	Asn	His	Phe	Asp	Ala	Gln	Ile	Phe
		515					520					525			
Thr	Pro	Asn	Tyr	Leu	Tyr	Asn	Ser	Asn	Gly	Asn	Leu	Ala	Thr	Arg	Pro
	530					535					540				
Lys	Ile	Thr	Arg	Thr	Ser	Thr	Gln	Ser	Val	Lys	Val	Gly	Gly	Arg	Ile
545					550					555					560
Thr	Ile	Ser	Thr	Asp	Ser	Ser	Ile	Ser	Lys	Ala	Ser	Leu	Ile	Arg	Tyr
				565					570					575	
Gly	Thr	Ala	Thr	His	Thr	Val	Asn	Thr	Asp	Gln	Arg	Arg	Ile	Pro	Leu
			580					585					590		
Thr	Leu	Thr	Asn	Asn	Gly	Gly	Asn	Ser	Tyr	Ser	Phe	Gln	Val	Pro	Ser
		595					600					605			
Asp	Ser	Gly	Val	Ala	Leu	Pro	Gly	Tyr	Trp	Met	Leu	Phe	Val	Met	Asn
	610					615					620				
Ser	Ala	Gly	Val	Pro	Ser	Val	Ala	Ser	Thr	Ile	Arg	Val	Thr	Gln	
625					630					635					

<210> 15

<211> 639

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant 11.03.10D6 (P136, T218, L312, V494A, N535D)
of *D. dendroides* GaO

<400> 15

Ala	Ser	Ala	Pro	Ile	Gly	Ser	Ala	Ile	Ser	Arg	Asn	Asn	Trp	Ala	Val
1				5				10						15	
Thr	Cys	Asp	Ser	Ala	Gln	Ser	Gly	Asn	Glu	Cys	Asn	Lys	Ala	Ile	Asp
			20					25					30		
Gly	Asn	Lys	Asp	Thr	Phe	Trp	His	Thr	Phe	Tyr	Gly	Ala	Asn	Gly	Asp
		35					40					45			
Pro	Lys	Pro	Pro	His	Thr	Tyr	Thr	Ile	Asp	Met	Lys	Thr	Thr	Gln	Asn
	50					55					60				
Val	Asn	Gly	Leu	Ser	Met	Leu	Pro	Arg	Gln	Asp	Gly	Asn	Gln	Asn	Gly
65					70					75					80
Trp	Ile	Gly	Arg	His	Glu	Val	Tyr	Leu	Ser	Ser	Asp	Gly	Thr	Asn	Trp
				85					90					95	
Gly	Ser	Pro	Val	Ala	Ser	Gly	Ser	Trp	Phe	Ala	Asp	Ser	Thr	Thr	Lys
			100					105					110		
Tyr	Ser	Asn	Phe	Glu	Thr	Arg	Pro	Ala	Arg	Tyr	Val	Arg	Leu	Val	Ala
		115					120					125			
Ile	Thr	Glu	Ala	Asn	Gly	Gln	Pro	Trp	Thr	Ser	Ile	Ala	Glu	Ile	Asn
	130					135					140				
Val	Phe	Gln	Ala	Ser	Ser	Tyr	Thr	Ala	Pro	Gln	Pro	Gly	Leu	Gly	Arg
145					150					155					160
Trp	Gly	Pro	Thr	Ile	Asp	Leu	Pro	Ile	Val	Pro	Ala	Ala	Ala	Ala	Ile
				165					170					175	
Glu	Pro	Thr	Ser	Gly	Arg	Val	Leu	Met	Trp	Ser	Ser	Tyr	Arg	Asn	Asp
			180					185					190		
Ala	Phe	Gly	Gly	Ser	Pro	Gly	Gly	Ile	Thr	Leu	Thr	Ser	Ser	Trp	Asp
	195						200					205			
Pro	Ser	Thr	Gly	Ile	Val	Ser	Asp	Arg	Thr	Val	Thr	Val	Thr	Lys	His
	210					215					220				
Asp	Met	Phe	Cys	Pro	Gly	Ile	Ser	Met	Asp	Gly	Asn	Gly	Gln	Ile	Val
225					230					235					240
Val	Thr	Gly	Gly	Asn	Asp	Ala	Lys	Lys	Thr	Ser	Leu	Tyr	Asp	Ser	Ser
				245					250					255	
Ser	Asp	Ser	Trp	Ile	Pro	Gly	Pro	Asp	Met	Gln	Val	Ala	Arg	Gly	Tyr
			260					265					270		
Gln	Ser	Ser	Ala	Thr	Met	Ser	Asp	Gly	Arg	Val	Phe	Thr	Ile	Gly	Gly
		275					280					285			
Ser	Trp	Ser	Gly	Gly	Val	Phe	Glu	Lys	Asn	Gly	Glu	Val	Tyr	Ser	Pro
	290					295					300				
Ser	Ser	Lys	Thr	Trp	Thr	Ser	Leu	Pro	Asn	Ala	Lys	Val	Asn	Pro	Met
305					310					315					320
Leu	Thr	Ala	Asp	Lys	Gln	Gly	Leu	Tyr	Arg	Ser	Asp	Asn	His	Ala	Trp
				325					330					335	
Leu	Phe	Gly	Trp	Lys	Lys	Gly	Ser	Val	Phe	Gln	Ala	Gly	Pro	Ser	Thr
			340					345					350		
Ala	Met	Asn	Trp	Tyr	Tyr	Thr	Ser	Gly	Ser	Gly	Asp	Val	Lys	Ser	Ala
		355					360					365			
Gly	Lys	Arg	Gln	Ser	Asn	Arg	Gly	Val	Ala	Pro	Asp	Ala	Met	Cys	Gly
	370					375					380				
Asn	Ala	Val	Met	Tyr	Asp	Ala	Val	Lys	Gly	Lys	Ile	Leu	Thr	Phe	Gly
385					390					395					400
Gly	Ser	Pro	Asp	Tyr	Gln	Asp	Ser	Asp	Ala	Thr	Thr	Asn	Ala	His	Ile

				405					410					415			
Ile	Thr	Leu	Gly	Glu	Pro	Gly	Thr	Ser	Pro	Asn	Thr	Val	Phe	Ala	Ser		
			420					425					430				
Asn	Gly	Leu	Tyr	Phe	Ala	Arg	Thr	Phe	His	Thr	Ser	Val	Val	Leu	Pro		
		435					440					445					
Asp	Gly	Ser	Thr	Phe	Ile	Thr	Gly	Gly	Gln	Arg	Arg	Gly	Ile	Pro	Phe		
	450					455					460						
Glu	Asp	Ser	Thr	Pro	Val	Phe	Thr	Pro	Glu	Ile	Tyr	Val	Pro	Glu	Gln		
465					470					475					480		
Asp	Thr	Phe	Tyr	Lys	Gln	Asn	Pro	Asn	Ser	Ile	Val	Arg	Ala	Tyr	His		
				485				490						495			
Ser	Ile	Ser	Leu	Leu	Leu	Pro	Asp	Gly	Arg	Val	Phe	Asn	Gly	Gly	Gly		
		500						505					510				
Gly	Leu	Cys	Gly	Asp	Cys	Thr	Thr	Asn	His	Phe	Asp	Ala	Gln	Ile	Phe		
	515					520						525					
Thr	Pro	Asn	Tyr	Leu	Tyr	Asp	Ser	Asn	Gly	Asn	Leu	Ala	Thr	Arg	Pro		
	530					535					540						
Lys	Ile	Thr	Arg	Thr	Ser	Thr	Gln	Ser	Val	Lys	Val	Gly	Gly	Arg	Ile		
545					550					555					560		
Thr	Ile	Ser	Thr	Asp	Ser	Ser	Ile	Ser	Lys	Ala	Ser	Leu	Ile	Arg	Tyr		
				565				570						575			
Gly	Thr	Ala	Thr	His	Thr	Val	Asn	Thr	Asp	Gln	Arg	Arg	Ile	Pro	Leu		
			580					585					590				
Thr	Leu	Thr	Asn	Asn	Gly	Gly	Asn	Ser	Tyr	Ser	Phe	Gln	Val	Pro	Ser		
	595					600					605						
Asp	Ser	Gly	Val	Ala	Leu	Pro	Gly	Tyr	Trp	Met	Leu	Phe	Val	Met	Asn		
	610					615				620							
Ser	Ala	Gly	Val	Pro	Ser	Val	Ala	Ser	Thr	Ile	Arg	Val	Thr	Gln			
625					630					635							

<210> 16
 <211> 639
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Mutant 11.03.13E12 (M70V, P136, V494A) from D.
 Dendroides GaO

				<400>													
Ala	Ser	Ala	Pro	Ile	Gly	Ser	Ala	Ile	Ser	Arg	Asn	Asn	Trp	Ala	Val		
1				5				10					15				
Thr	Cys	Asp	Ser	Ala	Gln	Ser	Gly	Asn	Glu	Cys	Asn	Lys	Ala	Ile	Asp		
		20					25					30					
Gly	Asn	Lys	Asp	Thr	Phe	Trp	His	Thr	Phe	Tyr	Gly	Ala	Asn	Gly	Asp		
	35					40					45						
Pro	Lys	Pro	Pro	His	Thr	Tyr	Thr	Ile	Asp	Met	Lys	Thr	Thr	Gln	Asn		
	50				55				60								
Val	Asn	Gly	Leu	Ser	Val	Leu	Pro	Arg	Gln	Asp	Gly	Asn	Gln	Asn	Gly		
65					70				75					80			
Trp	Ile	Gly	Arg	His	Glu	Val	Tyr	Leu	Ser	Ser	Asp	Gly	Thr	Asn	Trp		
				85				90						95			
Gly	Ser	Pro	Val	Ala	Ser	Gly	Ser	Trp	Phe	Ala	Asp	Ser	Thr	Thr	Lys		

			100					105				110					
Tyr	Ser	Asn	Phe	Glu	Thr	Arg	Pro	Ala	Arg	Tyr	Val	Arg	Leu	Val	Ala		
		115					120					125					
Ile	Thr	Glu	Ala	Asn	Gly	Gln	Pro	Trp	Thr	Ser	Ile	Ala	Glu	Ile	Asn		
	130					135					140						
Val	Phe	Gln	Ala	Ser	Ser	Tyr	Thr	Ala	Pro	Gln	Pro	Gly	Leu	Gly	Arg		
145				150						155					160		
Trp	Gly	Pro	Thr	Ile	Asp	Leu	Pro	Ile	Val	Pro	Ala	Ala	Ala	Ala	Ile		
			165						170					175			
Glu	Pro	Thr	Ser	Gly	Arg	Val	Leu	Met	Trp	Ser	Ser	Tyr	Arg	Asn	Asp		
		180						185					190				
Ala	Phe	Gly	Gly	Ser	Pro	Gly	Gly	Ile	Thr	Leu	Thr	Ser	Ser	Trp	Asp		
	195						200					205					
Pro	Ser	Thr	Gly	Ile	Val	Ser	Asp	Arg	Thr	Val	Thr	Val	Thr	Lys	His		
	210					215					220						
Asp	Met	Phe	Cys	Pro	Gly	Ile	Ser	Met	Asp	Gly	Asn	Gly	Gln	Ile	Val		
225				230						235					240		
Val	Thr	Gly	Gly	Asn	Asp	Ala	Lys	Lys	Thr	Ser	Leu	Tyr	Asp	Ser	Ser		
			245						250					255			
Ser	Asp	Ser	Trp	Ile	Pro	Gly	Pro	Asp	Met	Gln	Val	Ala	Arg	Gly	Tyr		
		260						265					270				
Gln	Ser	Ser	Ala	Thr	Met	Ser	Asp	Gly	Arg	Val	Phe	Thr	Ile	Gly	Gly		
	275					280						285					
Ser	Trp	Ser	Gly	Gly	Val	Phe	Glu	Lys	Asn	Gly	Glu	Val	Tyr	Ser	Pro		
	290				295						300						
Ser	Ser	Lys	Thr	Trp	Thr	Ser	Leu	Pro	Asn	Ala	Lys	Val	Asn	Pro	Met		
305				310						315					320		
Leu	Thr	Ala	Asp	Lys	Gln	Gly	Leu	Tyr	Arg	Ser	Asp	Asn	His	Ala	Trp		
			325						330					335			
Leu	Phe	Gly	Trp	Lys	Lys	Gly	Ser	Val	Phe	Gln	Ala	Gly	Pro	Ser	Thr		
		340						345					350				
Ala	Met	Asn	Trp	Tyr	Tyr	Thr	Ser	Gly	Ser	Gly	Asp	Val	Lys	Ser	Ala		
	355						360					365					
Gly	Lys	Arg	Gln	Ser	Asn	Arg	Gly	Val	Ala	Pro	Asp	Ala	Met	Cys	Gly		
	370					375					380						
Asn	Ala	Val	Met	Tyr	Asp	Ala	Val	Lys	Gly	Lys	Ile	Leu	Thr	Phe	Gly		
385				390						395					400		
Gly	Ser	Pro	Asp	Tyr	Gln	Asp	Ser	Asp	Ala	Thr	Thr	Asn	Ala	His	Ile		
			405						410					415			
Ile	Thr	Leu	Gly	Glu	Pro	Gly	Thr	Ser	Pro	Asn	Thr	Val	Phe	Ala	Ser		
		420						425					430				
Asn	Gly	Leu	Tyr	Phe	Ala	Arg	Thr	Phe	His	Thr	Ser	Val	Val	Leu	Pro		
		435					440					445					
Asp	Gly	Ser	Thr	Phe	Ile	Thr	Gly	Gly	Gln	Arg	Arg	Gly	Ile	Pro	Phe		
	450					455					460						
Glu	Asp	Ser	Thr	Pro	Val	Phe	Thr	Pro	Glu	Ile	Tyr	Val	Pro	Glu	Gln		
465				470						475					480		
Asp	Thr	Phe	Tyr	Lys	Gln	Asn	Pro	Asn	Ser	Ile	Val	Arg	Ala	Tyr	His		
			485					490						495			
Ser	Ile	Ser	Leu	Leu	Leu	Pro	Asp	Gly	Arg	Val	Phe	Asn	Gly	Gly	Gly		
		500						505					510				
Gly	Leu	Cys	Gly	Asp	Cys	Thr	Thr	Asn	His	Phe	Asp	Ala	Gln	Ile	Phe		
		515					520					525					

Thr	Pro	Asn	Tyr	Leu	Tyr	Asn	Ser	Asn	Gly	Asn	Leu	Ala	Thr	Arg	Pro
	530					535					540				
Lys	Ile	Thr	Arg	Thr	Ser	Thr	Gln	Ser	Val	Lys	Val	Gly	Gly	Arg	Ile
545					550					555					560
Thr	Ile	Ser	Thr	Asp	Ser	Ser	Ile	Ser	Lys	Ala	Ser	Leu	Ile	Arg	Tyr
				565					570					575	
Gly	Thr	Ala	Thr	His	Thr	Val	Asn	Thr	Asp	Gln	Arg	Arg	Ile	Pro	Leu
			580					585					590		
Thr	Leu	Thr	Asn	Asn	Gly	Gly	Asn	Ser	Tyr	Ser	Phe	Gln	Val	Pro	Ser
		595					600					605			
Asp	Ser	Gly	Val	Ala	Leu	Pro	Gly	Tyr	Trp	Met	Leu	Phe	Val	Met	Asn
	610					615					620				
Ser	Ala	Gly	Val	Pro	Ser	Val	Ala	Ser	Thr	Ile	Arg	Val	Thr	Gln	
625					630					635					

<210> 17

<211> 639

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant 1.06.20E7 (S10P, M70V, P136, G195E, V494A, N535D) from D. Dendroides GaO

<400> 17

Ala	Ser	Ala	Pro	Ile	Gly	Ser	Ala	Ile	Pro	Arg	Asn	Asn	Trp	Ala	Val
1				5					10					15	
Thr	Cys	Asp	Ser	Ala	Gln	Ser	Gly	Asn	Glu	Cys	Asn	Lys	Ala	Ile	Asp
		20					25					30			
Gly	Asn	Lys	Asp	Thr	Phe	Trp	His	Thr	Phe	Tyr	Gly	Ala	Asn	Gly	Asp
	35					40					45				
Pro	Lys	Pro	Pro	His	Thr	Tyr	Thr	Ile	Asp	Met	Lys	Thr	Thr	Gln	Asn
	50				55						60				
Val	Asn	Gly	Leu	Ser	Val	Leu	Pro	Arg	Gln	Asp	Gly	Asn	Gln	Asn	Gly
65					70				75					80	
Trp	Ile	Gly	Arg	His	Glu	Val	Tyr	Leu	Ser	Ser	Asp	Gly	Thr	Asn	Trp
			85				90						95		
Gly	Ser	Pro	Val	Ala	Ser	Gly	Ser	Trp	Phe	Ala	Asp	Ser	Thr	Thr	Lys
		100					105						110		
Tyr	Ser	Asn	Phe	Glu	Thr	Arg	Pro	Ala	Arg	Tyr	Val	Arg	Leu	Val	Ala
	115					120						125			
Ile	Thr	Glu	Ala	Asn	Gly	Gln	Pro	Trp	Thr	Ser	Ile	Ala	Glu	Ile	Asn
	130				135						140				
Val	Phe	Gln	Ala	Ser	Ser	Tyr	Thr	Ala	Pro	Gln	Pro	Gly	Leu	Gly	Arg
145					150					155					160
Trp	Gly	Pro	Thr	Ile	Asp	Leu	Pro	Ile	Val	Pro	Ala	Ala	Ala	Ala	Ile
				165					170					175	
Glu	Pro	Thr	Ser	Gly	Arg	Val	Leu	Met	Trp	Ser	Ser	Tyr	Arg	Asn	Asp
		180						185					190		
Ala	Phe	Glu	Gly	Ser	Pro	Gly	Gly	Ile	Thr	Leu	Thr	Ser	Ser	Trp	Asp
	195					200						205			
Pro	Ser	Thr	Gly	Ile	Val	Ser	Asp	Arg	Thr	Val	Thr	Val	Thr	Lys	His
	210					215						220			

Asp	Met	Phe	Cys	Pro	Gly	Ile	Ser	Met	Asp	Gly	Asn	Gly	Gln	Ile	Val
225					230					235					240
Val	Thr	Gly	Gly	Asn	Asp	Ala	Lys	Lys	Thr	Ser	Leu	Tyr	Asp	Ser	Ser
				245					250					255	
Ser	Asp	Ser	Trp	Ile	Pro	Gly	Pro	Asp	Met	Gln	Val	Ala	Arg	Gly	Tyr
			260					265					270		
Gln	Ser	Ser	Ala	Thr	Met	Ser	Asp	Gly	Arg	Val	Phe	Thr	Ile	Gly	Gly
		275					280					285			
Ser	Trp	Ser	Gly	Gly	Val	Phe	Glu	Lys	Asn	Gly	Glu	Val	Tyr	Ser	Pro
	290					295					300				
Ser	Ser	Lys	Thr	Trp	Thr	Ser	Leu	Pro	Asn	Ala	Lys	Val	Asn	Pro	Met
305					310					315					320
Leu	Thr	Ala	Asp	Lys	Gln	Gly	Leu	Tyr	Arg	Ser	Asp	Asn	His	Ala	Trp
				325					330					335	
Leu	Phe	Gly	Trp	Lys	Lys	Gly	Ser	Val	Phe	Gln	Ala	Gly	Pro	Ser	Thr
			340					345					350		
Ala	Met	Asn	Trp	Tyr	Tyr	Thr	Ser	Gly	Ser	Gly	Asp	Val	Lys	Ser	Ala
		355					360					365			
Gly	Lys	Arg	Gln	Ser	Asn	Arg	Gly	Val	Ala	Pro	Asp	Ala	Met	Cys	Gly
	370					375					380				
Asn	Ala	Val	Met	Tyr	Asp	Ala	Val	Lys	Gly	Lys	Ile	Leu	Thr	Phe	Gly
385					390					395					400
Gly	Ser	Pro	Asp	Tyr	Gln	Asp	Ser	Asp	Ala	Thr	Thr	Asn	Ala	His	Ile
				405					410					415	
Ile	Thr	Leu	Gly	Glu	Pro	Gly	Thr	Ser	Pro	Asn	Thr	Val	Phe	Ala	Ser
			420					425					430		
Asn	Gly	Leu	Tyr	Phe	Ala	Arg	Thr	Phe	His	Thr	Ser	Val	Val	Leu	Pro
		435					440					445			
Asp	Gly	Ser	Thr	Phe	Ile	Thr	Gly	Gly	Gln	Arg	Arg	Gly	Ile	Pro	Phe
	450					455					460				
Glu	Asp	Ser	Thr	Pro	Val	Phe	Thr	Pro	Glu	Ile	Tyr	Val	Pro	Glu	Gln
465					470					475					480
Asp	Thr	Phe	Tyr	Lys	Gln	Asn	Pro	Asn	Ser	Ile	Val	Arg	Ala	Tyr	His
				485					490					495	
Ser	Ile	Ser	Leu	Leu	Leu	Pro	Asp	Gly	Arg	Val	Phe	Asn	Gly	Gly	Gly
			500					505					510		
Gly	Leu	Cys	Gly	Asp	Cys	Thr	Thr	Asn	His	Phe	Asp	Ala	Gln	Ile	Phe
		515					520					525			
Thr	Pro	Asn	Tyr	Leu	Tyr	Asp	Ser	Asn	Gly	Asn	Leu	Ala	Thr	Arg	Pro
	530					535					540				
Lys	Ile	Thr	Arg	Thr	Ser	Thr	Gln	Ser	Val	Lys	Val	Gly	Gly	Arg	Ile
545					550					555					560
Thr	Ile	Ser	Thr	Asp	Ser	Ser	Ile	Ser	Lys	Ala	Ser	Leu	Ile	Arg	Tyr
				565					570					575	
Gly	Thr	Ala	Thr	His	Thr	Val	Asn	Thr	Asp	Gln	Arg	Arg	Ile	Pro	Leu
			580					585					590		
Thr	Leu	Thr	Asn	Asn	Gly	Gly	Asn	Ser	Tyr	Ser	Phe	Gln	Val	Pro	Ser
		595					600					605			
Asp	Ser	Gly	Val	Ala	Leu	Pro	Gly	Tyr	Trp	Met	Leu	Phe	Val	Met	Asn
	610					615					620				
Ser	Ala	Gly	Val	Pro	Ser	Val	Ala	Ser	Thr	Ile	Arg	Val	Thr	Gln	
625					630					635					

<210> 18
 <211> 639
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Mutant 1.D4 (N413D) from D. Dendroides GaO

<400> 18

Ala	Ser	Ala	Pro	Ile	Gly	Ser	Ala	Ile	Ser	Arg	Asn	Asn	Trp	Ala	Val
1				5				10					15		
Thr	Cys	Asp	Ser	Ala	Gln	Ser	Gly	Asn	Glu	Cys	Asn	Lys	Ala	Ile	Asp
			20					25					30		
Gly	Asn	Lys	Asp	Thr	Phe	Trp	His	Thr	Phe	Tyr	Gly	Ala	Asn	Gly	Asp
	35						40					45			
Pro	Lys	Pro	Pro	His	Thr	Tyr	Thr	Ile	Asp	Met	Lys	Thr	Thr	Gln	Asn
	50					55					60				
Val	Asn	Gly	Leu	Ser	Met	Leu	Pro	Arg	Gln	Asp	Gly	Asn	Gln	Asn	Gly
65					70					75					80
Trp	Ile	Gly	Arg	His	Glu	Val	Tyr	Leu	Ser	Ser	Asp	Gly	Thr	Asn	Trp
				85					90					95	
Gly	Ser	Pro	Val	Ala	Ser	Gly	Ser	Trp	Phe	Ala	Asp	Ser	Thr	Thr	Lys
			100					105					110		
Tyr	Ser	Asn	Phe	Glu	Thr	Arg	Pro	Ala	Arg	Tyr	Val	Arg	Leu	Val	Ala
		115					120					125			
Ile	Thr	Glu	Ala	Asn	Gly	Gln	Pro	Trp	Thr	Ser	Ile	Ala	Glu	Ile	Asn
	130					135					140				
Val	Phe	Gln	Ala	Ser	Ser	Tyr	Thr	Ala	Pro	Gln	Pro	Gly	Leu	Gly	Arg
145					150					155					160
Trp	Gly	Pro	Thr	Ile	Asp	Leu	Pro	Ile	Val	Pro	Ala	Ala	Ala	Ala	Ile
				165					170					175	
Glu	Pro	Thr	Ser	Gly	Arg	Val	Leu	Met	Trp	Ser	Ser	Tyr	Arg	Asn	Asp
			180					185					190		
Ala	Phe	Gly	Gly	Ser	Pro	Gly	Gly	Ile	Thr	Leu	Thr	Ser	Ser	Trp	Asp
		195					200					205			
Pro	Ser	Thr	Gly	Ile	Val	Ser	Asp	Arg	Thr	Val	Thr	Val	Thr	Lys	His
	210					215					220				
Asp	Met	Phe	Cys	Pro	Gly	Ile	Ser	Met	Asp	Gly	Asn	Gly	Gln	Ile	Val
225					230					235					240
Val	Thr	Gly	Gly	Asn	Asp	Ala	Lys	Lys	Thr	Ser	Leu	Tyr	Asp	Ser	Ser
				245					250					255	
Ser	Asp	Ser	Trp	Ile	Pro	Gly	Pro	Asp	Met	Gln	Val	Ala	Arg	Gly	Tyr
			260					265					270		
Gln	Ser	Ser	Ala	Thr	Met	Ser	Asp	Gly	Arg	Val	Phe	Thr	Ile	Gly	Gly
		275					280					285			
Ser	Trp	Ser	Gly	Gly	Val	Phe	Glu	Lys	Asn	Gly	Glu	Val	Tyr	Ser	Pro
	290					295					300				
Ser	Ser	Lys	Thr	Trp	Thr	Ser	Leu	Pro	Asn	Ala	Lys	Val	Asn	Pro	Met
305					310					315					320
Leu	Thr	Ala	Asp	Lys	Gln	Gly	Leu	Tyr	Arg	Ser	Asp	Asn	His	Ala	Trp
				325					330					335	
Leu	Phe	Gly	Trp	Lys	Lys	Gly	Ser	Val	Phe	Gln	Ala	Gly	Pro	Ser	Thr
			340					345					350		

Ala	Met	Asn	Trp	Tyr	Tyr	Thr	Ser	Gly	Ser	Gly	Asp	Val	Lys	Ser	Ala
		355					360					365			
Gly	Lys	Arg	Gln	Ser	Asn	Arg	Gly	Val	Ala	Pro	Asp	Ala	Met	Cys	Gly
	370					375					380				
Asn	Ala	Val	Met	Tyr	Asp	Ala	Val	Lys	Gly	Lys	Ile	Leu	Thr	Phe	Gly
385					390					395					400
Gly	Ser	Pro	Asp	Tyr	Gln	Asp	Ser	Asp	Ala	Thr	Thr	Asp	Ala	His	Ile
			405					410						415	
Ile	Thr	Leu	Gly	Glu	Pro	Gly	Thr	Ser	Pro	Asn	Thr	Val	Phe	Ala	Ser
			420					425					430		
Asn	Gly	Leu	Tyr	Phe	Ala	Arg	Thr	Phe	His	Thr	Ser	Val	Val	Leu	Pro
		435					440					445			
Asp	Gly	Ser	Thr	Phe	Ile	Thr	Gly	Gly	Gln	Arg	Arg	Gly	Ile	Pro	Phe
	450					455					460				
Glu	Asp	Ser	Thr	Pro	Val	Phe	Thr	Pro	Glu	Ile	Tyr	Val	Pro	Glu	Gln
465					470					475					480
Asp	Thr	Phe	Tyr	Lys	Gln	Asn	Pro	Asn	Ser	Ile	Val	Arg	Val	Tyr	His
			485						490					495	
Ser	Ile	Ser	Leu	Leu	Leu	Pro	Asp	Gly	Arg	Val	Phe	Asn	Gly	Gly	Gly
			500					505					510		
Gly	Leu	Cys	Gly	Asp	Cys	Thr	Thr	Asn	His	Phe	Asp	Ala	Gln	Ile	Phe
		515					520					525			
Thr	Pro	Asn	Tyr	Leu	Tyr	Asn	Ser	Asn	Gly	Asn	Leu	Ala	Thr	Arg	Pro
	530					535					540				
Lys	Ile	Thr	Arg	Thr	Ser	Thr	Gln	Ser	Val	Lys	Val	Gly	Gly	Arg	Ile
545					550					555					560
Thr	Ile	Ser	Thr	Asp	Ser	Ser	Ile	Ser	Lys	Ala	Ser	Leu	Ile	Arg	Tyr
			565						570					575	
Gly	Thr	Ala	Thr	His	Thr	Val	Asn	Thr	Asp	Gln	Arg	Arg	Ile	Pro	Leu
			580					585					590		
Thr	Leu	Thr	Asn	Asn	Gly	Gly	Asn	Ser	Tyr	Ser	Phe	Gln	Val	Pro	Ser
		595					600					605			
Asp	Ser	Gly	Val	Ala	Leu	Pro	Gly	Tyr	Trp	Met	Leu	Phe	Val	Met	Asn
	610					615					620				
Ser	Ala	Gly	Val	Pro	Ser	Val	Ala	Ser	Thr	Ile	Arg	Val	Thr	Gln	
625					630					635					

<210> 19

<211> 639

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant 2.G4 (N413D, S550) from D. Dendroides GaO

<400> 19

Ala	Ser	Ala	Pro	Ile	Gly	Ser	Ala	Ile	Ser	Arg	Asn	Asn	Trp	Ala	Val
1				5				10					15		
Thr	Cys	Asp	Ser	Ala	Gln	Ser	Gly	Asn	Glu	Cys	Asn	Lys	Ala	Ile	Asp
			20					25					30		
Gly	Asn	Lys	Asp	Thr	Phe	Trp	His	Thr	Phe	Tyr	Gly	Ala	Asn	Gly	Asp
		35					40					45			
Pro	Lys	Pro	Pro	His	Thr	Tyr	Thr	Ile	Asp	Met	Lys	Thr	Thr	Gln	Asn

50	Val	Asn	Gly	Leu	Ser	Met	55	Leu	Pro	Arg	Gln	Asp	60	Gly	Asn	Gln	Asn	Gly
65	Trp	Ile	Gly	Arg	His	70	Glu	Val	Tyr	Leu	Ser	75	Ser	Asp	Gly	Thr	Asn	Trp
					85		Ser	Gly	Ser	Trp	Phe	90	Ala	Asp	Ser	Thr	Thr	Lys
	Gly	Ser	Pro	Val	Ala	100				105						110		
	Tyr	Ser	Asn	Phe	Glu	115	Thr	Arg	Pro	Ala	Arg	Tyr	Val	Arg	Leu	Val	Ala	
									120					125				
	Ile	Thr	Glu	Ala	Asn	130	Gly	Gln	Pro	Trp	Thr	Ser	Ile	Ala	Glu	Ile	Asn	
								135						140				
	Val	Phe	Gln	Ala	Ser	145	Ser	Tyr	Thr	Ala	Pro	Gln	Pro	Gly	Leu	Gly	Arg	
								150				155					160	
	Trp	Gly	Pro	Thr	Ile	165	Asp	Leu	Pro	Ile	Val	Pro	Ala	Ala	Ala	Ala	Ile	
											170					175		
	Glu	Pro	Thr	Ser	Gly	180	Arg	Val	Leu	Met	Trp	Ser	Ser	Tyr	Arg	Asn	Asp	
										185					190			
	Ala	Phe	Gly	Gly	Ser	195	Pro	Gly	Gly	Ile	Thr	Leu	Thr	Ser	Ser	Trp	Asp	
									200					205				
	Pro	Ser	Thr	Gly	Ile	210	Val	Ser	Asp	Arg	Thr	Val	Thr	Val	Thr	Lys	His	
								215						220				
	Asp	Met	Phe	Cys	Pro	225	Gly	Ile	Ser	Met	Asp	Gly	Asn	Gly	Gln	Ile	Val	
								230				235					240	
	Val	Thr	Gly	Gly	Asn	245	Asp	Ala	Lys	Lys	Thr	Ser	Leu	Tyr	Asp	Ser	Ser	
											250				255			
	Ser	Asp	Ser	Trp	Ile	260	Pro	Gly	Pro	Asp	Met	Gln	Val	Ala	Arg	Gly	Tyr	
										265					270			
	Gln	Ser	Ser	Ala	Thr	275	Met	Ser	Asp	Gly	Arg	Val	Phe	Thr	Ile	Gly	Gly	
									280					285				
	Ser	Trp	Ser	Gly	Gly	290	Val	Phe	Glu	Lys	Asn	Gly	Glu	Val	Tyr	Ser	Pro	
								295				300						
	Ser	Ser	Lys	Thr	Trp	305	Thr	Ser	Leu	Pro	Asn	Ala	Lys	Val	Asn	Pro	Met	
								310				315				320		
	Leu	Thr	Ala	Asp	Lys	325	Gln	Gly	Leu	Tyr	Arg	Ser	Asp	Asn	His	Ala	Trp	
											330				335			
	Leu	Phe	Gly	Trp	Lys	340	Lys	Gly	Ser	Val	Phe	Gln	Ala	Gly	Pro	Ser	Thr	
										345				350				
	Ala	Met	Asn	Trp	Tyr	355	Tyr	Thr	Ser	Gly	Ser	Gly	Asp	Val	Lys	Ser	Ala	
									360					365				
	Gly	Lys	Arg	Gln	Ser	370	Asn	Arg	Gly	Val	Ala	Pro	Asp	Ala	Met	Cys	Gly	
								375				380						
	Asn	Ala	Val	Met	Tyr	385	Asp	Ala	Val	Lys	Gly	Lys	Ile	Leu	Thr	Phe	Gly	
								390				395					400	
	Gly	Ser	Pro	Asp	Tyr	405	Gln	Asp	Ser	Asp	Ala	Thr	Thr	Asp	Ala	His	Ile	
											410				415			
	Ile	Thr	Leu	Gly	Glu	420	Pro	Gly	Thr	Ser	Pro	Asn	Thr	Val	Phe	Ala	Ser	
										425				430				
	Asn	Gly	Leu	Tyr	Phe	435	Ala	Arg	Thr	Phe	His	Thr	Ser	Val	Val	Leu	Pro	
									440					445				
	Asp	Gly	Ser	Thr	Phe	450	Ile	Thr	Gly	Gly	Gln	Arg	Arg	Gly	Ile	Pro	Phe	
								455				460						
	Glu	Asp	Ser	Thr	Pro	465	Val	Phe	Thr	Pro	Glu	Ile	Tyr	Val	Pro	Glu	Gln	
								470				475					480	

Asp	Thr	Phe	Tyr	Lys	Gln	Asn	Pro	Asn	Ser	Ile	Val	Arg	Val	Tyr	His
				485					490					495	
Ser	Ile	Ser	Leu	Leu	Leu	Pro	Asp	Gly	Arg	Val	Phe	Asn	Gly	Gly	Gly
			500					505					510		
Gly	Leu	Cys	Gly	Asp	Cys	Thr	Thr	Asn	His	Phe	Asp	Ala	Gln	Ile	Phe
		515					520					525			
Thr	Pro	Asn	Tyr	Leu	Tyr	Asn	Ser	Asn	Gly	Asn	Leu	Ala	Thr	Arg	Pro
	530					535					540				
Lys	Ile	Thr	Arg	Thr	Ser	Thr	Gln	Ser	Val	Lys	Val	Gly	Gly	Arg	Ile
545					550					555					560
Thr	Ile	Ser	Thr	Asp	Ser	Ser	Ile	Ser	Lys	Ala	Ser	Leu	Ile	Arg	Tyr
				565					570					575	
Gly	Thr	Ala	Thr	His	Thr	Val	Asn	Thr	Asp	Gln	Arg	Arg	Ile	Pro	Leu
			580					585					590		
Thr	Leu	Thr	Asn	Asn	Gly	Gly	Asn	Ser	Tyr	Ser	Phe	Gln	Val	Pro	Ser
		595					600					605			
Asp	Ser	Gly	Val	Ala	Leu	Pro	Gly	Tyr	Trp	Met	Leu	Phe	Val	Met	Asn
	610					615					620				
Ser	Ala	Gly	Val	Pro	Ser	Val	Ala	Ser	Thr	Ile	Arg	Val	Thr	Gln	
625					630					635					

<210> 20

<211> 639

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant 3.H7 (N413D, S550, V494A) from D.
Dendroides GaO

<400> 20

Ala	Ser	Ala	Pro	Ile	Gly	Ser	Ala	Ile	Ser	Arg	Asn	Asn	Trp	Ala	Val
1				5					10					15	
Thr	Cys	Asp	Ser	Ala	Gln	Ser	Gly	Asn	Glu	Cys	Asn	Lys	Ala	Ile	Asp
		20					25					30			
Gly	Asn	Lys	Asp	Thr	Phe	Trp	His	Thr	Phe	Tyr	Gly	Ala	Asn	Gly	Asp
	35					40					45				
Pro	Lys	Pro	Pro	His	Thr	Tyr	Thr	Ile	Asp	Met	Lys	Thr	Thr	Gln	Asn
	50				55						60				
Val	Asn	Gly	Leu	Ser	Met	Leu	Pro	Arg	Gln	Asp	Gly	Asn	Gln	Asn	Gly
65					70				75						80
Trp	Ile	Gly	Arg	His	Glu	Val	Tyr	Leu	Ser	Asp	Gly	Thr	Asn	Trp	
				85				90					95		
Gly	Ser	Pro	Val	Ala	Ser	Gly	Ser	Trp	Phe	Ala	Asp	Ser	Thr	Thr	Lys
		100					105						110		
Tyr	Ser	Asn	Phe	Glu	Thr	Arg	Pro	Ala	Arg	Tyr	Val	Arg	Leu	Val	Ala
		115					120					125			
Ile	Thr	Glu	Ala	Asn	Gly	Gln	Pro	Trp	Thr	Ser	Ile	Ala	Glu	Ile	Asn
	130					135					140				
Val	Phe	Gln	Ala	Ser	Ser	Tyr	Thr	Ala	Pro	Gln	Pro	Gly	Leu	Gly	Arg
145					150					155					160
Trp	Gly	Pro	Thr	Ile	Asp	Leu	Pro	Ile	Val	Pro	Ala	Ala	Ala	Ala	Ile
				165					170					175	

Glu	Pro	Thr	Ser	Gly	Arg	Val	Leu	Met	Trp	Ser	Ser	Tyr	Arg	Asn	Asp
			180					185					190		
Ala	Phe	Gly	Gly	Ser	Pro	Gly	Gly	Ile	Thr	Leu	Thr	Ser	Ser	Trp	Asp
		195					200					205			
Pro	Ser	Thr	Gly	Ile	Val	Ser	Asp	Arg	Thr	Val	Thr	Val	Thr	Lys	His
	210					215					220				
Asp	Met	Phe	Cys	Pro	Gly	Ile	Ser	Met	Asp	Gly	Asn	Gly	Gln	Ile	Val
225					230					235					240
Val	Thr	Gly	Gly	Asn	Asp	Ala	Lys	Lys	Thr	Ser	Leu	Tyr	Asp	Ser	Ser
				245					250					255	
Ser	Asp	Ser	Trp	Ile	Pro	Gly	Pro	Asp	Met	Gln	Val	Ala	Arg	Gly	Tyr
			260					265					270		
Gln	Ser	Ser	Ala	Thr	Met	Ser	Asp	Gly	Arg	Val	Phe	Thr	Ile	Gly	Gly
		275					280					285			
Ser	Trp	Ser	Gly	Gly	Val	Phe	Glu	Lys	Asn	Gly	Glu	Val	Tyr	Ser	Pro
	290					295					300				
Ser	Ser	Lys	Thr	Trp	Thr	Ser	Leu	Pro	Asn	Ala	Lys	Val	Asn	Pro	Met
305					310					315					320
Leu	Thr	Ala	Asp	Lys	Gln	Gly	Leu	Tyr	Arg	Ser	Asp	Asn	His	Ala	Trp
				325					330					335	
Leu	Phe	Gly	Trp	Lys	Lys	Gly	Ser	Val	Phe	Gln	Ala	Gly	Pro	Ser	Thr
			340					345					350		
Ala	Met	Asn	Trp	Tyr	Tyr	Thr	Ser	Gly	Ser	Gly	Asp	Val	Lys	Ser	Ala
		355					360					365			
Gly	Lys	Arg	Gln	Ser	Asn	Arg	Gly	Val	Ala	Pro	Asp	Ala	Met	Cys	Gly
	370					375					380				
Asn	Ala	Val	Met	Tyr	Asp	Ala	Val	Lys	Gly	Lys	Ile	Leu	Thr	Phe	Gly
385					390					395					400
Gly	Ser	Pro	Asp	Tyr	Gln	Asp	Ser	Asp	Ala	Thr	Thr	Asp	Ala	His	Ile
				405					410					415	
Ile	Thr	Leu	Gly	Glu	Pro	Gly	Thr	Ser	Pro	Asn	Thr	Val	Phe	Ala	Ser
			420					425					430		
Asn	Gly	Leu	Tyr	Phe	Ala	Arg	Thr	Phe	His	Thr	Ser	Val	Val	Leu	Pro
		435					440					445			
Asp	Gly	Ser	Thr	Phe	Ile	Thr	Gly	Gly	Gln	Arg	Arg	Gly	Ile	Pro	Phe
	450					455					460				
Glu	Asp	Ser	Thr	Pro	Val	Phe	Thr	Pro	Glu	Ile	Tyr	Val	Pro	Glu	Gln
465					470					475					480
Asp	Thr	Phe	Tyr	Lys	Gln	Asn	Pro	Asn	Ser	Ile	Val	Arg	Ala	Tyr	His
				485					490					495	
Ser	Ile	Ser	Leu	Leu	Leu	Pro	Asp	Gly	Arg	Val	Phe	Asn	Gly	Gly	Gly
			500					505					510		
Gly	Leu	Cys	Gly	Asp	Cys	Thr	Thr	Asn	His	Phe	Asp	Ala	Gln	Ile	Phe
		515					520					525			
Thr	Pro	Asn	Tyr	Leu	Tyr	Asn	Ser	Asn	Gly	Asn	Leu	Ala	Thr	Arg	Pro
	530					535						540			
Lys	Ile	Thr	Arg	Thr	Ser	Thr	Gln	Ser	Val	Lys	Val	Gly	Gly	Arg	Ile
545					550					555					560
Thr	Ile	Ser	Thr	Asp	Ser	Ser	Ile	Ser	Lys	Ala	Ser	Leu	Ile	Arg	Tyr
				565					570					575	
Gly	Thr	Ala	Thr	His	Thr	Val	Asn	Thr	Asp	Gln	Arg	Arg	Ile	Pro	Leu
			580					585					590		
Thr	Leu	Thr	Asn	Asn	Gly	Gly	Asn	Ser	Tyr	Ser	Phe	Gln	Val	Pro	Ser

	595		600		605
Asp	Ser Gly Val Ala Leu Pro Gly Tyr Trp Met Leu Phe Val Met Asn				
610		615		620	
Ser	Ala Gly Val Pro Ser Val Ala Ser Thr Ile Arg Val Thr Gln				
625		630		635	

<210> 21
 <211> 639
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Mutant 4.F12 (N413D, S550, V494A, S610) from D.
 Dendroides GaO

<400> 21

Ala	Ser	Ala	Pro	Ile	Gly	Ser	Ala	Ile	Ser	Arg	Asn	Asn	Trp	Ala	Val
1				5					10					15	
Thr	Cys	Asp	Ser	Ala	Gln	Ser	Gly	Asn	Glu	Cys	Asn	Lys	Ala	Ile	Asp
			20					25					30		
Gly	Asn	Lys	Asp	Thr	Phe	Trp	His	Thr	Phe	Tyr	Gly	Ala	Asn	Gly	Asp
		35					40					45			
Pro	Lys	Pro	Pro	His	Thr	Tyr	Thr	Ile	Asp	Met	Lys	Thr	Thr	Gln	Asn
	50					55					60				
Val	Asn	Gly	Leu	Ser	Met	Leu	Pro	Arg	Gln	Asp	Gly	Asn	Gln	Asn	Gly
65					70					75					80
Trp	Ile	Gly	Arg	His	Glu	Val	Tyr	Leu	Ser	Ser	Asp	Gly	Thr	Asn	Trp
				85					90					95	
Gly	Ser	Pro	Val	Ala	Ser	Gly	Ser	Trp	Phe	Ala	Asp	Ser	Thr	Thr	Lys
			100					105					110		
Tyr	Ser	Asn	Phe	Glu	Thr	Arg	Pro	Ala	Arg	Tyr	Val	Arg	Leu	Val	Ala
		115					120					125			
Ile	Thr	Glu	Ala	Asn	Gly	Gln	Pro	Trp	Thr	Ser	Ile	Ala	Glu	Ile	Asn
	130					135					140				
Val	Phe	Gln	Ala	Ser	Ser	Tyr	Thr	Ala	Pro	Gln	Pro	Gly	Leu	Gly	Arg
145					150					155					160
Trp	Gly	Pro	Thr	Ile	Asp	Leu	Pro	Ile	Val	Pro	Ala	Ala	Ala	Ala	Ile
				165					170					175	
Glu	Pro	Thr	Ser	Gly	Arg	Val	Leu	Met	Trp	Ser	Ser	Tyr	Arg	Asn	Asp
			180					185					190		
Ala	Phe	Gly	Gly	Ser	Pro	Gly	Gly	Ile	Thr	Leu	Thr	Ser	Ser	Trp	Asp
		195					200					205			
Pro	Ser	Thr	Gly	Ile	Val	Ser	Asp	Arg	Thr	Val	Thr	Val	Thr	Lys	His
	210					215					220				
Asp	Met	Phe	Cys	Pro	Gly	Ile	Ser	Met	Asp	Gly	Asn	Gly	Gln	Ile	Val
225					230					235					240
Val	Thr	Gly	Gly	Asn	Asp	Ala	Lys	Lys	Thr	Ser	Leu	Tyr	Asp	Ser	Ser
				245					250					255	
Ser	Asp	Ser	Trp	Ile	Pro	Gly	Pro	Asp	Met	Gln	Val	Ala	Arg	Gly	Tyr
			260					265					270		
Gln	Ser	Ser	Ala	Thr	Met	Ser	Asp	Gly	Arg	Val	Phe	Thr	Ile	Gly	Gly
		275					280					285			
Ser	Trp	Ser	Gly	Gly	Val	Phe	Glu	Lys	Asn	Gly	Glu	Val	Tyr	Ser	Pro

290	Ser	Ser	Lys	Thr	Trp	Thr	Ser	Leu	Pro	Asn	Ala	Lys	Val	Asn	Pro	Met
305						310					315					320
	Leu	Thr	Ala	Asp	Lys	Gln	Gly	Leu	Tyr	Arg	Ser	Asp	Asn	His	Ala	Trp
					325					330					335	
	Leu	Phe	Gly	Trp	Lys	Lys	Gly	Ser	Val	Phe	Gln	Ala	Gly	Pro	Ser	Thr
				340					345					350		
	Ala	Met	Asn	Trp	Tyr	Tyr	Thr	Ser	Gly	Ser	Gly	Asp	Val	Lys	Ser	Ala
			355					360					365			
	Gly	Lys	Arg	Gln	Ser	Asn	Arg	Gly	Val	Ala	Pro	Asp	Ala	Met	Cys	Gly
		370				375						380				
	Asn	Ala	Val	Met	Tyr	Asp	Ala	Val	Lys	Gly	Lys	Ile	Leu	Thr	Phe	Gly
385					390						395					400
	Gly	Ser	Pro	Asp	Tyr	Gln	Asp	Ser	Asp	Ala	Thr	Thr	Asp	Ala	His	Ile
				405					410						415	
	Ile	Thr	Leu	Gly	Glu	Pro	Gly	Thr	Ser	Pro	Asn	Thr	Val	Phe	Ala	Ser
			420					425					430			
	Asn	Gly	Leu	Tyr	Phe	Ala	Arg	Thr	Phe	His	Thr	Ser	Val	Val	Leu	Pro
		435					440						445			
	Asp	Gly	Ser	Thr	Phe	Ile	Thr	Gly	Gly	Gln	Arg	Arg	Gly	Ile	Pro	Phe
		450				455					460					
	Glu	Asp	Ser	Thr	Pro	Val	Phe	Thr	Pro	Glu	Ile	Tyr	Val	Pro	Glu	Gln
465					470						475					480
	Asp	Thr	Phe	Tyr	Lys	Gln	Asn	Pro	Asn	Ser	Ile	Val	Arg	Ala	Tyr	His
				485					490						495	
	Ser	Ile	Ser	Leu	Leu	Pro	Asp	Gly	Arg	Val	Phe	Asn	Gly	Gly	Gly	
			500				505						510			
	Gly	Leu	Cys	Gly	Asp	Cys	Thr	Thr	Asn	His	Phe	Asp	Ala	Gln	Ile	Phe
		515					520						525			
	Thr	Pro	Asn	Tyr	Leu	Tyr	Asn	Ser	Asn	Gly	Asn	Leu	Ala	Thr	Arg	Pro
		530				535						540				
	Lys	Ile	Thr	Arg	Thr	Ser	Thr	Gln	Ser	Val	Lys	Val	Gly	Gly	Arg	Ile
545					550						555					560
	Thr	Ile	Ser	Thr	Asp	Ser	Ser	Ile	Ser	Lys	Ala	Ser	Leu	Ile	Arg	Tyr
				565					570						575	
	Gly	Thr	Ala	Thr	His	Thr	Val	Asn	Thr	Asp	Gln	Arg	Arg	Ile	Pro	Leu
			580					585					590			
	Thr	Leu	Thr	Asn	Asn	Gly	Gly	Asn	Ser	Tyr	Ser	Phe	Gln	Val	Pro	Ser
		595				600						605				
	Asp	Ser	Gly	Val	Ala	Leu	Pro	Gly	Tyr	Trp	Met	Leu	Phe	Val	Met	Asn
		610				615					620					
	Ser	Ala	Gly	Val	Pro	Ser	Val	Ala	Ser	Thr	Ile	Arg	Val	Thr	Gln	
625					630						635					

<210> 22
 <211> 10
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Vector sequence

<400> 22

aagctagctt	10
<210> 23	
<211> 10	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Vector sequence	
<400> 23	
ttcgatcgaa	10
<210> 24	
<211> 10	
<212> DNA	
<213> Artificial Sequence	
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gaattaattc	10
<210> 25	
<211> 10	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Vector sequence	
<400> 25	
cttaattaag	10
<210> 26	
<211> 9	
<212> PRT	
<213> Dactylium dendroides	
<400> 26	
Met Ala Ser Ala Pro Ile Gly Ser Ala	
1 5	
<210> 27	
<211> 27	
<212> DNA	
<213> Dactylium dendroides	
<400> 27	
atggcctcag cacctatcgg aagcgcc	27
<210> 28	

<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<221> unsure
<222> (1)...(27)
<223> "n" at positions 6, 9, 12, 15, and 21 is either a,
t, g, or c.
"n" at position 18 is either a, t, or c.

<223> Randomly altered D. Dendoides wild-type sequence

<400> 28
atggcntcng cncchnatngg nagcgcc

27

<210> 29
<211> 14
<212> DNA
<213> Artificial Sequence

<220>
<223> Vector sequence

<400> 29
aggaaaagct tatg

14

<210> 30
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Vector sequence

<400> 30
aggaaaaagc ttatg

15

<210> 31
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Vector sequence

<400> 31
aggaaacaag cttatg

16

<210> 32
<211> 16
<212> DNA
<213> Artificial Sequence

<220>		
<223>	Vector sequence	
<400>	32	
aggaacaaag	cttatg	16
<210>	33	
<211>	14	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Vector sequence	
<400>	33	
aggaaaagct	tatg	14
<210>	34	
<211>	15	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Vector sequence	
<400>	34	
aggaaaaagc	ttatg	15
<210>	35	
<211>	16	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Vector sequence	
<400>	35	
aggaaacaag	cttatg	16
<210>	36	
<211>	16	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Vector sequence	
<400>	36	
aggaacaaag	cttatg	16
<210>	37	
<211>	1917	

<212> DNA

<213> Artificial Sequence

<220>

<223> Mutant 9.16.8D2 (A1609G) of D. Dendroides GaO

<400> 37

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gcacagtcgg	gaaatgaatg	caacaaggcc	attgatggca	acaaggatac	cttttggcac	120
acattctatg	gcgccaacgg	ggatccaaag	ccccctcaca	catacacgat	tgacatgaag	180
acaactcaga	acgtcaacgg	cttgtctatg	ctgcctcgac	aggatggtaa	ccaaaacggc	240
tggatcggtc	gccatgaggt	ttatctaagc	tcagatggca	caaactgggg	cagccctggt	300
gcgtcaggta	gttggttcgc	cgactctact	acaaaatact	ccaactttga	aactcgccct	360
gctcgctatg	ttcgtcttgt	cgctatcact	gaagcgaatg	gccagccttg	gactagcatt	420
gcagagatca	acgtcttcca	agctagtctt	tacacagccc	cccagcctgg	tcttggacgc	480
tgggggtccga	ctattgactt	accgattggt	cctgcggctg	cagcaattga	accgacatcg	540
ggacgagtc	ttatgtggtc	ttcatatcgc	aatgatgcat	ttggaggatc	ccctgggtggt	600
atcactttga	cgtcttctcg	ggatccatcc	actgggtattg	tttccgaccg	cactgtgaca	660
gtcaccaagc	atgatatggt	ctgccctggt	atctccatgg	atggtaacgg	tcagatcgta	720
gtcacagggtg	gcaacgatgc	caagaagacc	agtttgtatg	attcatctag	cgatagctgg	780
atcccgggac	ctgacatgca	agtggctcgt	gggtatcagt	catcagctac	catgtcagac	840
ggtcgtgttt	ttaccattgg	aggctcctgg	agcgggtggcg	tatttgagaa	gaatggcgaa	900
gtctatagcc	catcttcaaa	gacatggacg	tccctaccca	atgccaaagg	caacccaatg	960
ttgacggctg	acaagcaagg	attgtaccgt	tcagacaacc	acgcgtggct	ctttggatgg	1020
aagaagggtt	cgggtgtcca	agcgggacct	agcacagcca	tgaactggta	ctataccagt	1080
ggaagtgggtg	atgtgaagtc	agccggaaaa	cgccagtcta	accgtgggtg	agccccctgat	1140
gccatgtgcg	gaaacgctgt	catgtacgac	gccgttaaag	gaaagatcct	gacctttggc	1200
ggctccccag	attatcaaga	ctctgacgcc	acaaccaacg	cccacatcat	caccctcggt	1260
gaacccggaa	catctcccaa	cactgtcttt	gctagcaatg	ggttgtactt	tgcccgaacg	1320
tttcacacct	ctgttggtct	tccagacgga	agcacgttta	ttacaggagg	ccaacgacgt	1380
ggaattccgt	tcgaggattc	aaccccggtg	tttacacctg	agatctacgt	ccctgaacaa	1440
gacactttct	acaagcagaa	ccccaaactcc	attgttcgcg	tctaccatag	catttccctt	1500
ttgttacctg	atggcaggggt	atttaacggt	ggtggtggtc	tttgtggcga	ttgtaccacg	1560
aatcattttcg	acgcgcaaat	ctttacgcc	aactatcttt	acaatagcga	cggcaatctc	1620
gcgacacgtc	ccaagattac	cagaacctct	acacagagcg	tcaagggtcgg	tggcagaatt	1680
acaatctcga	cggattcttc	gattagcaag	gcgtcgttga	ttcgctatgg	tacagcgaca	1740
cacacggtta	atactgacca	gcgccgcatt	cccctgactc	tgacaaacaa	tggaggaaat	1800
agctattctt	tccaagttcc	tagecactct	ggtgttgctt	tgcttggtta	ctggatgttg	1860
ttcgtgatga	actcggccgg	tgttcctagt	gtggcttcga	cgattcgcgt	tactcag	1917

<210> 38

<211> 1917

<212> DNA

<213> Artificial Sequence

<220>

<223> Mutant 9.16.6C11 (T1481C, T1543A) of D. Dendroides
GaO

<400> 38

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gcacagtcgg	gaaatgaatg	caacaaggcc	attgatggca	acaaggatac	cttttggcac	120
acattctatg	gcgccaacgg	ggatccaaag	ccccctcaca	catacacgat	tgacatgaag	180

acaactcaga	acgtcaacgg	cttgtctatg	ctgcctcgac	aggatggtaa	ccaaaacggc	240
tggatcggtc	gccatgaggt	ttatctaagc	tcagatggca	caaactgggg	cagccctggt	300
gcgtcaggta	gttggttcgc	cgactctact	acaaaatact	ccaactttga	aactcgcctt	360
gctcgctatg	ttcgtcttgt	cgctatcact	gaagcgaatg	gccagccttg	gactagcatt	420
gcagagatca	acgtcttcca	agctagtctt	tacacagccc	cccagcctgg	tcttggacgc	480
tgggggtccga	ctattgactt	accgattggt	cctgcggctg	cagcaattga	accgacatcg	540
ggacgagtc	ttatgtggtc	ttcatatcgc	aatgatgcat	ttggaggatc	ccctgggtggt	600
atcactttga	cgtcttcttg	ggatccatcc	actggtattg	tttccgaccg	cactgtgaca	660
gtcaccaagc	atgatatggt	ctgccctggt	atctccatgg	atggtaacgg	tcagatcgta	720
gtcacagggtg	gcaacgatgc	caagaagacc	agtttgtatg	attcatctag	cgatagctgg	780
atccccgggac	ctgacatgca	agtggctcgt	gggtatcagt	catcagctac	catgtcagac	840
ggtcgtgttt	ttaccattgg	aggctcctgg	agcgggtggc	tatttgagaa	gaatggcgaa	900
gtctatagcc	catcttcaaa	gacatggacg	tccctaccca	atgccaaagg	caacccaatg	960
ttgacggctg	acaagcaagg	attgtaccgt	tcagacaacc	acgcgtgggt	ctttggatgg	1020
aagaagggtt	cggtgttcca	agcgggacct	agcacagcca	tgaactggta	ctataccagt	1080
ggaagtgggtg	atgtgaagtc	agccggaaaa	cgccagtcta	accgtgggtg	agccccgat	1140
gccatgtgcg	gaaacgctgt	catgtacgac	gccgttaaag	gaaagatcct	gacctttggc	1200
ggctccccag	attatcaaga	ctctgacgcc	acaaccaacg	cccacatcat	caccctcgg	1260
gaacccggaa	catctcccaa	cactgtcttt	gctagcaatg	ggttgtactt	tgcccgaacg	1320
tttcacacct	ctgttggtct	tccagacgga	agcacgttta	ttacaggagg	ccaacgacgt	1380
ggaattccgt	tcgaggattc	aaccccggta	tttacacctg	agatctacgt	ccctgaacaa	1440
gacactttct	acaagcagaa	ccccaaactcc	attgttcgcg	cctaccatag	catttccctt	1500
ttgttacctg	atggcagggt	atttaacggt	ggtggtgggt	ttagtggcga	ttgtaccacg	1560
aatcatttcg	acgcgcaa	ctttacgcca	aactatcttt	acaatagcaa	cggcaatctc	1620
gcgacacgtc	ccaagattac	cagaacctct	acacagagcg	tcaagggtcgg	tggcagaatt	1680
acaatctcga	cggattcttc	gattagcaag	gcgtcgttga	ttcgctatgg	tacagcgaca	1740
cacacgggtta	atactgacca	gcgccgcatt	cccctgactc	tgacaaacaa	tggaggaaat	1800
agctattctt	tccaagttcc	tagcgactct	ggtgttgctt	tgcctggcta	ctggatgttg	1860
ttcgtgatga	actcggccgg	tgttcctagt	gtggcttcga	cgattcgcgt	tactcag	1917

<210> 39

<211> 1917

<212> DNA

<213> Artificial Sequence

<220>

<223> Mutant 9.16.16D12 (T408C, T1481C) of D. Dendroides
GaO

<400> 39

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gcacagtcgg	gaaatgaatg	caacaaggcc	attgatggca	acaaggatac	cttttggcac	120
acattctatg	gcgccaacgg	ggatccaaag	ccccctcaca	catacacgat	tgacatgaag	180
acaactcaga	acgtcaacgg	cttgtctatg	ctgcctcgac	aggatggtaa	ccaaaacggc	240
tggatcggtc	gccatgaggt	ttatctaagc	tcagatggca	caaactgggg	cagccctggt	300
gcgtcaggta	gttggttcgc	cgactctact	acaaaatact	ccaactttga	aactcgcctt	360
gctcgctatg	ttcgtcttgt	cgctatcact	gaagcgaatg	gccagccctg	gactagcatt	420
gcagagatca	acgtcttcca	agctagtctt	tacacagccc	cccagcctgg	tcttggacgc	480
tgggggtccga	ctattgactt	accgattggt	cctgcggctg	cagcaattga	accgacatcg	540
ggacgagtc	ttatgtggtc	ttcatatcgc	aatgatgcat	ttggaggatc	ccctgggtggt	600
atcactttga	cgtcttcttg	ggatccatcc	actggtattg	tttccgaccg	cactgtgaca	660
gtcaccaagc	atgatatggt	ctgccctggt	atctccatgg	atggtaacgg	tcagatcgta	720
gtcacagggtg	gcaacgatgc	caagaagacc	agtttgtatg	attcatctag	cgatagctgg	780

atccccgggac	ctgacatgca	agtggctcgt	gggtatcagt	catcagctac	catgtcagac	840
ggtcgtgttt	ttaccattgg	aggctcctgg	agcgggtggcg	tatttgagaa	gaatggcgaa	900
gtctatagcc	catcttcaaa	gacatggacg	tccttaccba	atgccaaagg	caacccaatg	960
ttgacggctg	acaagcaagg	attgtaccgt	tcagacaacc	acgcgtggct	ctttggatgg	1020
aagaagggtt	cggtgttcca	agcgggacct	agcacagcca	tgaactggta	ctataccagt	1080
ggaagtgggtg	atgtgaagtc	agccggaaaa	cgccagtcta	accgtgggtg	agccccctgat	1140
gccatgtgcg	gaaacgctgt	catgtacgac	gccgttaaag	gaaagatcct	gaccttttggc	1200
ggctccccag	attatcaaga	ctctgacgcc	acaaccaacg	cccacatcat	caccctcggt	1260
gaacccggaa	catctcccaa	cactgtcttt	gctagcaatg	ggttgtactt	tgcccgaacg	1320
tttcacacct	ctgttggttct	tccagacgga	agcacgttta	ttacaggagg	ccaacgacgt	1380
ggaattccgt	tcgaggattc	aaccccggtg	tttacacctg	agatctacgt	ccctgaacaa	1440
gacactttct	acaagcagaa	ccccaaactcc	attgttcgcg	cctaccatag	cattttccctt	1500
ttgttacctg	atggcagggt	atttaacggg	gggtgggtggtc	tttgtggcga	ttgtaccacg	1560
aatcattttcg	acgcgcgaaat	ctttacgcca	aactatcttt	acaatagcaa	cggcaatctc	1620
gcgacacgtc	ccaagattac	cagaacctct	acacagagcg	tcaagggtcg	tggcagaatt	1680
acaatctcga	cggattcttc	gattagcaag	gcgtcggttg	ttcgctatgg	tacagcgaca	1740
cacacgggta	atactgacca	gcgcgcgatt	cccctgactc	tgacaaacaa	tggagggaat	1800
agctattctt	tccaagttcc	tagcgactct	gggtgttgctt	tgcttggtta	ctggatgttg	1860
ttcgtgatga	actcggccgg	tgttcctagt	gtggcttcga	cgattcgcgt	tactcag	1917

<210> 40

<211> 1917

<212> DNA

<213> Artificial Sequence

<220>

<223> Mutant 11.03.6D3 (T28C, T408C, T1481C) of D.
Dendroides GaO

<400> 40

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gcacagtcgg	gaaatgaatg	caacaaggcc	attgatggca	acaaggatac	cttttggcac	120
acattctatg	gcgccaacgg	ggatccaaag	ccccctcaca	catacacgat	tgacatgaag	180
acaactcaga	acgtcaacgg	cttgtctatg	ctgcctcgac	aggatggtaa	ccaaaacggc	240
tggatcggtc	gccatgaggt	ttatctaagc	tcagatggca	caaactgggg	cagccctggt	300
gcgtcaggta	gttggttcgc	cgactctact	acaaaatact	ccaactttga	aactcgcctt	360
gctcgctatg	ttcgtcttgt	cgctatcact	gaagcgaatg	gccagccctg	gactagcatt	420
gcagagatca	acgtcttcca	agctagtctt	tacacagccc	cccagccctg	tcttggacgc	480
tgggggtccga	ctattgactt	accgattggt	cctgcggctg	cagcaattga	accgacatcg	540
ggacgagtc	ttatgtgggt	ttcatatcgc	aatgatgcat	ttggaggatc	ccctgggtggt	600
atcactttga	cgtcttctctg	ggatccatcc	actggtattg	tttccgaccg	cactgtgaca	660
gtcaccaagc	atgatatggt	ctgccctggt	atctccatgg	atggtaacgg	tcagatcgta	720
gtcacagggtg	gcaacgatgc	caagaagacc	agtttgtatg	attcatctag	cgatagctgg	780
atccccgggac	ctgacatgca	agtggctcgt	gggtatcagt	catcagctac	catgtcagac	840
ggtcgtgttt	ttaccattgg	aggctcctgg	agcgggtggcg	tatttgagaa	gaatggcgaa	900
gtctatagcc	catcttcaaa	gacatggacg	tccttaccba	atgccaaagg	caacccaatg	960
ttgacggctg	acaagcaagg	attgtaccgt	tcagacaacc	acgcgtggct	ctttggatgg	1020
aagaagggtt	cggtgttcca	agcgggacct	agcacagcca	tgaactggta	ctataccagt	1080
ggaagtgggtg	atgtgaagtc	agccggaaaa	cgccagtcta	accgtgggtg	agccccctgat	1140
gccatgtgcg	gaaacgctgt	catgtacgac	gccgttaaag	gaaagatcct	gaccttttggc	1200
ggctccccag	attatcaaga	ctctgacgcc	acaaccaacg	cccacatcat	caccctcggt	1260
gaacccggaa	catctcccaa	cactgtcttt	gctagcaatg	ggttgtactt	tgcccgaacg	1320
tttcacacct	ctgttggttct	tccagacgga	agcacgttta	ttacaggagg	ccaacgacgt	1380

ggaattccgt	tcgaggattc	aacccccggt	tttacacctg	agatctacgt	ccctgaacaa	1440
gacactttct	acaagcagaa	cccccaactcc	attgttcgcg	cctaccatag	catttccctt	1500
ttgttacctg	atggcagggg	atttaacggg	gggtgggtg	tttgtggcga	ttgtaccacg	1560
aatcatttgc	acgcgcaa	ctttacgcca	aactatcttt	acaatagcaa	cggcaatctc	1620
gcgacacg	ccaagattac	cagaacctct	acacagagcg	tcaagggtcg	tggcagaatt	1680
acaatctcga	cggattcttc	gattagcaag	gcgtcggtga	ttcgctatgg	tacagcgaca	1740
cacacgggta	atactgacca	gcgcgcgatt	cccctgactc	tgacaaacaa	tggaggaaat	1800
agctattctt	tccaagttcc	tagcgactct	gggtgttgct	tgccctggcta	ctggatgttg	1860
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<210> 41

<211> 1917

<212> DNA

<213> Artificial Sequence

<220>

<223> Mutant 11.03.10C3 (A9C, T408C, G584A, T1481C) of
D. Dendroides GaO

<400> 41

gcctcagccc	ctatcggaag	cgccatttct	cgcaacaact	gggccggtcac	ttgcgacagt	60
gcacagtcgg	gaaatgaatg	caacaaggcc	attgatggca	acaaggatac	cttttggcac	120
acatttctatg	gcgccaacgg	ggatccaaag	ccccctcaca	catacacgat	tgacatgaag	180
acaactcaga	acgtcaacgg	cttgtctatg	ctgcctcgac	aggatggtaa	ccaaaacggc	240
tggatcggtc	gccatgaggt	ttatctaagc	tcagatggca	caaactgggg	cagccctggt	300
gcgtcaggta	gttggttcgc	cgactctact	acaaaatact	ccaactttga	aactcgcctt	360
gctcgctatg	ttcgtcttgt	cgctatcact	gaagcgaatg	gccagccctg	gactagcatt	420
gcagagatca	acgtcttcca	agctagtctt	tacacagccc	cccagcctgg	tcttggacgc	480
tgggggtccga	ctattgactt	accgattggt	cctgcggctg	cagcaattga	accgacatcg	540
ggacgagtc	ttatgtgggc	ttcatatcgc	aatgatgc	ttgaaggatc	ccctgggtggt	600
atcactttga	cgtcttctctg	ggatccatcc	actggtattg	tttccgaccg	cactgtgaca	660
gtcaccaagc	atgatatggt	ctgccttggt	atctccatgg	atggtaacgg	tcagatcgta	720
gtcacagggtg	gcaacgatgc	caagaagacc	agtttgtatg	attcatctag	cgatagctgg	780
atcccggggac	ctgacatgca	agtggctcgt	gggtatcagt	catcagctac	catgtcagac	840
ggtcgtgttt	ttaccattgg	aggctcctgg	agcgggtggc	tatttgagaa	gaatggcgaa	900
gtctatagcc	catcttcaaa	gacatggacg	tccctaccca	atgccaaagg	caacccaatg	960
ttgacgggtg	acaagcaagg	attgtaccgt	tcagacaacc	acgcgtgggt	ctttggatgg	1020
aagaaggggt	cgggtgttcca	agcggggacct	agcacagcca	tgaactggta	ctataccagt	1080
ggaagtgggtg	atgtgaagtc	agccggaaaa	cgccagtcta	accgtgggtg	agccccctgat	1140
gccatgtgcg	gaaacgctgt	catgtacgac	gccgttaaag	gaaagatcct	gacctttggc	1200
ggctccccag	attatcaaga	ctctgacgcc	acaaccaacg	cccacatcat	caccctcggt	1260
gaacccggaa	catctcccaa	cactgtcttt	gctagcaatg	ggttgtactt	tgcccgaacg	1320
tttcacacct	ctgttggttct	tccagacgga	agcacgttta	ttacaggagg	ccaacgacgt	1380
ggaattccgt	tcgaggattc	aacccccggt	tttacacctg	agatctacgt	ccctgaacaa	1440
gacactttct	acaagcagaa	cccccaactcc	attgttcgcg	cctaccatag	catttccctt	1500
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acaatctcga	cggattcttc	gattagcaag	gcgtcggtga	ttcgctatgg	tacagcgaca	1740
cacacgggta	atactgacca	gcgcgcgatt	cccctgactc	tgacaaacaa	tggaggaaat	1800
agctattctt	tccaagttcc	tagcgactct	gggtgttgct	tgccctggcta	ctggatgttg	1860
ttcgtgatga	actcggccgg	tggttcctagt	gtggcttcga	cgattcgcgt	tactcag	1917

<210> 42
 <211> 1917
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Mutant 11.03.10D6 (T408C, T654C, A936G, T1481C, A1603G) of D. Dendroides GaO

<400> 42

gcctcagcac	ctatcggaag	cgccatttct	cgcaacaact	gggccgtcac	ttgcgacagt	60
gcacagtcgg	gaaatgaatg	caacaaggcc	attgatggca	acaaggatac	cttttggcac	120
acattctatg	gcgccaacgg	ggatccaaag	ccccctcaca	catacacgat	tgacatgaag	180
acaactcaga	acgtcaacgg	cttgtctatg	ctgcctcgac	aggatggtaa	ccaaaacggc	240
tggatcggtc	gccatgaggt	ttatctaagc	tcagatggca	caaactgggg	cagccctggt	300
gcgtcaggta	gttgggttcgc	cgactctact	acaaaatact	ccaactttga	aactcgccct	360
gctcgctatg	ttcgtcttgt	cgctatcact	gaagcgaatg	gccagccctg	gactagcatt	420
gcagagatca	acgtcttcca	agctagttct	tacacagccc	cccagccctg	tcttggacgc	480
tgggggtccga	ctattgactt	accgattggt	cctgcggctg	cagcaattga	accgacatcg	540
ggacgagtc	ttatgtggtc	ttcatatcgc	aatgatgcat	ttggaggatc	ccctgggtggt	600
atcactttga	cgtcttccctg	ggatccatcc	actggtattg	tttccgaccg	caccgtgaca	660
gtcaccaagc	atgatatggt	ctgccttggt	atctccatgg	atggtaacgg	tcagatcgta	720
gtcacagggtg	gcaacgatgc	caagaagacc	agtttgtatg	attcatctag	cgatagctgg	780
atcccggggac	ctgacatgca	agtggctcgt	gggtatcagt	catcagctac	catgtcagac	840
ggtcgtgttt	ttaccattgg	aggctcctgg	agcgggtggc	tatttgagaa	gaatggcgaa	900
gtctatagcc	catcttcaaa	gacatggacg	tccctgccca	atgccaaagg	caacccaatg	960
ttgacggctg	acaagcaagg	attgtaccgt	tcagacaacc	acgcgtggct	ctttggatgg	1020
aagaagggtt	cggtgttcca	agcgggacct	agcacagcca	tgaactggta	ctataccagt	1080
ggaagtgggtg	atgtgaagtc	agccggaaaa	cgccagtcta	accgtgggtg	agccccctgat	1140
gccatgtgcg	gaaacgctgt	catgtacgac	gccgttaaag	gaaagatcct	gacctttggc	1200
ggctccccag	attatcaaga	ctctgacgcc	acaaccaacg	cccacatcat	caccctcggt	1260
gaacccggaa	catctcccaa	cactgtcttt	gctagcaatg	ggttgtactt	tgcccgaacg	1320
tttcacacct	ctgttggtct	tccagacgga	agcacgttta	ttacaggagg	ccaacgacgt	1380
ggaattccgt	tcgaggattc	aaccccggta	tttacacctg	agatctacgt	ccctgaacaa	1440
gacactttct	acaagcagaa	ccccaaactcc	attgttcgcg	cctaccatag	catttccctt	1500
ttgttacctg	atggcaggggt	atttaacgggt	gggtggtggc	tttgtggcga	ttgtaccacg	1560
aatcatttcg	acgcgcaa	ctttacgcca	aactatcttt	acgatagcaa	cggcaatctc	1620
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agctattctt	tccaagttcc	tagcgactct	gggtgttgct	tgcttggtta	ctggatgttg	1860
ttcgtgatga	actcggccgg	tgttcctagt	gtggcttcga	cgattcgcgt	tactcag	1917

<210> 43
 <211> 1917
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Mutant 11.03.13E12 (A208G, T408C, T1481C) of D. Dendroides GaO

<400> 43

gcctcagcac	ctatcggaag	cgccatttct	cgcaacaact	gggccggtcac	ttgcgacagt	60
gcacagtcgg	gaaatgaatg	caacaaggcc	attgatggca	acaaggatac	cttttggcac	120
acattctatg	gcgccaacgg	ggatccaaag	ccccctcaca	catacacgat	tgacatgaag	180
acaactcaga	acgtcaacgg	cttgtctgtg	ctgcctcgac	aggatggtaa	ccaaaacggc	240
tggatcggtc	gccatgaggt	ttatctaagc	tcagatggca	caaactgggg	cagccctggt	300
gcgtcaggta	gttgggttcgc	cgactctact	acaaaatact	ccaactttga	aactcgccct	360
gctcgctatg	ttcgtcttgt	cgctatcact	gaagegaatg	gccagccctg	gactagcatt	420
gcagagatca	acgtcttcca	agctagtctt	tacacagccc	cccagcctgg	tcttggacgc	480
tgggggtccga	ctattgactt	accgattggt	cctgcggctg	cagcaattga	accgacatcg	540
ggacgagtc	ttatgtggtc	ttcatatcgc	aatgatgcat	ttggaggatc	ccctgggtggt	600
atcactttga	cgtcttctcg	ggatccatcc	actgggtattg	tttccgaccg	cactgtgaca	660
gtcaccaagc	atgatatggt	ctgccctggg	atctccatgg	atggtaacgg	tcagatcgta	720
gtcacagggtg	gcaacgatgc	caagaagacc	agtttgtatg	attcatctag	cgatagctgg	780
atcccgggac	ctgacatgca	agtggctcgt	gggtatcagt	catcagctac	catgtcagac	840
ggtcgtgttt	ttaccattgg	aggctcctgg	agcgggtggcg	tatttgagaa	gaatggcgaa	900
gtctatagcc	catcttcaaa	gacatggacg	tccctaccca	atgccaaagt	caacccaatg	960
ttgacggctg	acaagcaagg	attgtaccgt	tcagacaacc	acgcgtggct	ctttggatgg	1020
aagaagggtt	cggtgttcca	agcgggacct	agcacagcca	tgaactggta	ctataccagt	1080
ggaagtgggtg	atgtgaagtc	agccggaaaa	cgccagtccta	accgtgggtg	agccctgat	1140
gccatgtgcg	gaaacgctgt	catgtacgac	gccgttaaag	gaaagatcct	gacctttggc	1200
ggctccccag	attatcaaga	ctctgacgcc	acaaccaacg	cccacatcat	cacctcgggt	1260
gaacccggaa	catctcccaa	cactgtcttt	gctagcaatg	ggttgtactt	tgcccgaacg	1320
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ggaattccgt	tcgaggattc	aaccccggta	tttacacctg	agatctacgt	ccctgaacaa	1440
gacactttct	acaagcagaa	ccccaaactcc	attgttcgcg	cctaccatag	catttccctt	1500
ttgttaacctg	atggcaggggt	atttaacgggt	gggtgggtggc	tttgtggcga	ttgtaccacg	1560
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cacacgggtta	atactgacca	gcgccgcatt	cccctgactc	tgacaaacaa	tggaggaaat	1800
agctattctt	tccaagttcc	tagcgactct	gggtgttgctt	tgcttggtta	ctggatgttg	1860
ttcgtgatga	actcggccgg	tgttcctagt	gtggcttcga	cgattcgcgt	tactcag	1917

<210> 44

<211> 1917

<212> DNA

<213> Artificial Sequence

<220>

<223> Mutant 1.06.20E7 (T28C, A208G, T408C, G584A, T1481C, A1603G) of D. Dendroides GaO

<400> 44

gcctcagcac	ctatcggaag	cgccattcct	cgcaacaact	gggccggtcac	ttgcgacagt	60
gcacagtcgg	gaaatgaatg	caacaaggcc	attgatggca	acaaggatac	cttttggcac	120
acattctatg	gcgccaacgg	ggatccaaag	ccccctcaca	catacacgat	tgacatgaag	180
acaactcaga	acgtcaacgg	cttgtctgtg	ctgcctcgac	aggatggtaa	ccaaaacggc	240
tggatcggtc	gccatgaggt	ttatctaagc	tcagatggca	caaactgggg	cagccctggt	300
gcgtcaggta	gttgggttcgc	cgactctact	acaaaatact	ccaactttga	aactcgccct	360
gctcgctatg	ttcgtcttgt	cgctatcact	gaagegaatg	gccagccctg	gactagcatt	420
gcagagatca	acgtcttcca	agctagtctt	tacacagccc	cccagcctgg	tcttggacgc	480
tgggggtccga	ctattgactt	accgattggt	cctgcggctg	cagcaattga	accgacatcg	540
ggacgagtc	ttatgtggtc	ttcatatcgc	aatgatgcat	ttgaaggatc	ccctgggtggt	600

atcactttga	cgtcttctg	ggatccatcc	actggtattg	tttccgaccg	cactgtgaca	660
gtcaccaagc	atgatatgtt	ctgccctggt	atctccatgg	atggtaacgg	tcagatcgta	720
gtcacagggtg	gcaacgatgc	caagaagacc	agtttgtatg	attcatctag	cgatagctgg	780
atcccgggac	ctgacatgca	agtggctcgt	gggtatcagt	catcagctac	catgtcagac	840
ggtcgtgttt	ttaccattgg	aggctcctgg	agcgggtggcg	tatttgagaa	gaatggcgaa	900
gtctatagcc	catcttcaaa	gacatggacg	tccttaccga	atgccaaagg	caacccaatg	960
ttgacggctg	acaagcaagg	attgtaccgt	tcagacaacc	acgcgtgggt	ctttggatgg	1020
aagaaggggt	cgggtgttcca	agcgggacct	agcacagcca	tgaactggta	ctataccagt	1080
ggaagtgggtg	atgtgaagtc	agccggaaaa	cgccagtcta	accgtgggtg	agccccctgat	1140
gccatgtgcg	gaaacgctgt	catgtacgac	gccgttaaag	gaaagatcct	gacctttggc	1200
ggctccccag	attatcaaga	ctctgacgcc	acaaccaacg	cccacatcat	caccctcggt	1260
gaacccggaa	catctcccaa	cactgtcttt	gctagcaatg	ggttgtactt	tgcccgaaag	1320
tttcacacct	ctgttggtct	tcagacggga	agcacgttta	ttacaggagg	ccaacgacgt	1380
ggaattccgt	tcgaggattc	aaccccggtg	tttacacctg	agatctacgt	ccctgaacaa	1440
gacactttct	acaagcagaa	ccccaaactcc	attgttcgcg	cctaccatag	catttccctt	1500
ttgttacctg	atggcagggg	atttaacggg	gggtggtggc	tttgtggcga	ttgtaccacg	1560
aatcatttcg	acgcgcaaag	ctttacgcca	aactatcttt	acgatagcaa	cggcaatctc	1620
gcgacacgtc	ccaagattac	cagaacctct	acacagagcg	tcaaggtcgg	tggcagaatt	1680
acaatctcga	cggattcttc	gattagcaag	gcgtcgttga	ttcgctatgg	tacagcgaca	1740
cacacgggta	atactgacca	gcgcgcgatt	cccttgactc	tgacaaacaa	tggaggaaat	1800
agctattctt	tccaagttcc	tagcgactct	gggtgtgctt	tgcttggtga	ctggatgttg	1860
ttcgtgatga	actcggcggg	tgttcctagt	gtggcttcga	cgattcgcgt	tactcag	1917

<210> 45

<211> 1917

<212> DNA

<213> Artificial Sequence

<220>

<223> Mutant 1.D4 (A1237G) of D. Dendroides GaO

<400> 45

gcctcagcac	ctatcggaag	cgccatttct	cgcaacaact	gggccgtcac	ttgcgacagt	60
gcacagtcgg	gaaatgaatg	caacaaggcc	attgatggca	acaaggatac	cttttggcac	120
acattctatg	gcgccaacgg	ggatccaaag	ccccctcaca	catacacgat	tgacatgaag	180
acaactcaga	acgtcaacgg	cttgtctatg	ctgcctcgac	aggatggtaa	ccaaaacggc	240
tggatcggtc	gccatgaggt	ttatctaagc	tcagatggca	caaactgggg	cagccctgtt	300
gcgtcaggta	gttgggttcg	cgactctact	acaaaatact	ccaactttga	aactcgcctt	360
gctcgctatg	ttcgtcttgt	cgctatcact	gaagcgaatg	gccagccttg	gactagcatt	420
gcagagatca	acgtcttcca	agctagtctt	tacacagccc	cccagcctgg	tcttggacgc	480
tgggggtccga	ctattgactt	accgattgtt	cctgcggctg	cagcaattga	accgacatcg	540
ggacgagtc	ttatgtgggt	ttcatatcgc	aatgatgcat	ttggaggatc	ccctgggtgg	600
atcactttga	cgtcttctg	ggatccatcc	actggtattg	tttccgaccg	cactgtgaca	660
gtcaccaagc	atgatatgtt	ctgccctggt	atctccatgg	atggtaacgg	tcagatcgta	720
gtcacagggtg	gcaacgatgc	caagaagacc	agtttgtatg	attcatctag	cgatagctgg	780
atcccgggac	ctgacatgca	agtggctcgt	gggtatcagt	catcagctac	catgtcagac	840
ggtcgtgttt	ttaccattgg	aggctcctgg	agcgggtggcg	tatttgagaa	gaatggcgaa	900
gtctatagcc	catcttcaaa	gacatggacg	tccttaccga	atgccaaagg	caacccaatg	960
ttgacggctg	acaagcaagg	attgtaccgt	tcagacaacc	acgcgtgggt	ctttggatgg	1020
aagaaggggt	cgggtgttcca	agcgggacct	agcacagcca	tgaactggta	ctataccagt	1080
ggaagtgggtg	atgtgaagtc	agccggaaaa	cgccagtcta	accgtgggtg	agccccctgat	1140
gccatgtgcg	gaaacgctgt	catgtacgac	gccgttaaag	gaaagatcct	gacctttggc	1200
ggctccccag	attatcaaga	ctctgacgcc	acaaccgacg	cccacatcat	caccctcggt	1260

gaaccgga	catctccaa	cactgtcttt	gctagcaatg	ggttgtaact	tgccgaacg	1320
tttcacacct	ctgttggttct	tccagacgga	agcacgttta	ttacaggagg	ccaacgacgt	1380
ggaattccgt	tcgaggattc	aaccggtta	tttacacctg	agatctacgt	ccctgaacaa	1440
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ttgttacctg	atggcagggt	atttaacggt	ggtgggtggtc	tttgtggcga	ttgtaccacg	1560
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gcgacacgtc	ccaagattac	cagaacctct	acacagagcg	tcaaggtcgg	tggcagaatt	1680
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cacacgggta	atactgacca	gcgcgcgcat	cccctgactc	tgacaaacaa	tggaggaaat	1800
agctattctt	tccaagttcc	tagcgactct	ggtgttgctt	tgcttggtta	ctggatgttg	1860
ttcgtgatga	actcggcggg	tgttcctagt	gtggcttcga	cgattcgcgt	tactcag	1917

<210> 46

<211> 1917

<212> DNA

<213> Artificial Sequence

<220>

<223> Mutant 2.G4 (A1237G, T1650A) of D. Dendroides GaO

<400> 46

gcctcagcac	ctatcggaag	cgccatttct	cgcaacaact	gggccgtcac	ttgcgacagt	60
gcacagtcgg	gaaatgaatg	caacaaggcc	attgatggca	acaaggatac	cttttggcac	120
acattctatg	gcgccaacgg	ggatccaaag	ccccctcaca	catacacgat	tgacatgaag	180
acaactcaga	acgtcaacgg	cttgtctatg	ctgcctcgac	aggatggtaa	ccaaaacggc	240
tggatcgggtc	gccatgaggt	ttatctaage	tcagatggca	caaactgggg	cagccctgtt	300
gcgtcaggta	gttggttcgc	cgactctact	acaaaataact	ccaactttga	aactcgcctt	360
gctcgctatg	ttcgtcttgt	cgctatcact	gaagcgaatg	gccagccttg	gactagcatt	420
gcagagatca	acgtcttcca	agctagttct	tacacagccc	cccagcctgg	tcttggacgc	480
tggggtccga	ctattgactt	accgattgtt	cctgcggctg	cagcaattga	accgacatcg	540
ggacgagtc	ttatgtggtc	ttcatatcgc	aatgatgcat	ttggaggatc	ccctgggtgt	600
atcactttga	cgtcttctctg	ggatccatcc	actgggtattg	tttccgaccg	cactgtgaca	660
gtcaccaagc	atgatatgtt	ctgccctggg	atctccatgg	atggtaacgg	tcagatcgta	720
gtcacagggtg	gcaacgatgc	caagaagacc	agtttgtatg	attcatctag	cgatagctgg	780
atcccggggac	ctgacatgca	agtggctcgt	gggtatcagt	catcagctac	catgtcagac	840
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gtctatagcc	catcttcaaa	gacatggacg	tccttaccca	atgccaaagg	caaccatg	960
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aagaagggtt	cgggtgtcca	agcgggacct	agcacagcca	tgaactggta	ctataccagt	1080
ggaagtgggtg	atgtgaagtc	agccggaaaa	cgccagctta	accgtgggtg	agcccctgat	1140
gccatgtgcg	gaaacgctgt	catgtacgac	gccgttaaag	gaaagatcct	gacctttggc	1200
ggctccccag	attatcaaga	ctctgacgcc	acaaccgacg	cccacatcat	caccctcggt	1260
gaaccgga	catctccaa	cactgtcttt	gctagcaatg	ggttgtaact	tgccgaacg	1320
tttcacacct	ctgttggttct	tccagacgga	agcacgttta	ttacaggagg	ccaacgacgt	1380
ggaattccgt	tcgaggattc	aaccggtta	tttacacctg	agatctacgt	ccctgaacaa	1440
gacactttct	acaagcagaa	ccccaaactcc	attgttcgcg	tctaccatag	catttccctt	1500
ttgttacctg	atggcagggt	atttaacggt	ggtgggtggtc	tttgtggcga	ttgtaccacg	1560
aatcatttcg	acgcgcaa	ctttacgcca	aactatcttt	acaatagcaa	cggcaatctc	1620
gcgacacgtc	ccaagattac	cagaacctca	acacagagcg	tcaaggtcgg	tggcagaatt	1680
acaatctcga	cggattcttc	gattagcaag	gcgtcggtga	ttcgctatgg	tacagcgaca	1740
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agctattctt	tccaagttcc	tagcgactct	ggtgttgctt	tgcttggtta	ctggatgttg	1860
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<210> 47
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 <212> DNA
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<220>
 <223> Mutant 3.H7 (A1237G, T1650A, T1481C) of D.
 Dendroides GaO

<400> 47

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<210> 48
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<220>
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